

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:17 ; Search time 117 Seconds

(without alignments)
1637.343 Million cell updates/sec

Title: US-10-761-593a-18

Perfect score: 2323
Sequence: 1 MGWHECPAWLWLLSLSLP.....MHKALHNYTKSLSPGK 436

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	436	7 ADM33853	Adm33853 Human HuE
2	2323	100.0	436	8 ADP48984	Adp48984 HuEPO-L-P
3	2323	100.0	436	8 ADM47516	Adm47516 Human EPO
4	2323	100.0	436	9 AEA18933	Aea18933 Human ery
5	2323	100.0	436	9 AEA88753	Aea88753 Human ery
6	2216.5	95.4	435	7 ADM33857	Adm33857 Human HuE
7	2216.5	95.4	435	8 ADP48988	Adp48988 HuEPO-L-V
8	2216.5	95.4	435	8 ADM47520	Adm47520 Human EPO
9	2216.5	95.4	435	9 AEA18937	Aea18937 Human ery
10	2216.5	95.4	435	9 AEA88757	Aea88757 Human ery
11	2212.5	95.2	437	7 ADM33855	Adm33855 Human HuE
12	2212.5	95.2	437	8 ADP48986	Adp48986 HuEPO-L-V
13	2212.5	95.2	437	8 ADM47518	Adm47518 Human EPO
14	2212.5	95.2	437	9 AEA18935	Aea18935 Human ery
15	2212.5	95.2	437	9 AEA88755	Aea88755 Human ery
16	2168.5	93.3	441	9 AEB70229	Aeb70229 EPO analo
17	2108	90.7	428	8 ABU64200	Abu64200 Plasmid P
18	2108	90.7	428	8 ADO10513	Ado10513 EPO signa
19	2108	90.7	428	8 ADV97050	Adv97050 Human Ery
20	2058	88.6	428	5 AAE15348	Aae15348 Human ery
21	1958.5	84.3	425	7 ABU64199	Abu64199 Plasmid P
22	1958.5	84.3	425	8 ADO10511	Ado10511 Kb signal
23	1929	83.0	444	9 ADV97042	Adv97042 Human EPO
24	1348.5	58.0	448	7 ADM33376	Adm33376 Human GCS

25	1348.5	58.0	448	9 ADV91791	Adv91791 Human GCS
26	1348.5	58.0	448	9 ADV99712	Adv99712 hg-CSF-L-
27	1347	58.0	432	8 ADM50823	Adm50823 Human int
28	1264.5	54.4	408	8 ADQ95471	Adq95471 Fusion pr
29	1264.5	54.4	408	8 ADQ95473	Adq95473 Fusion pr
30	1262.5	53.5	469	9 AEA5895	Aea5895 Human mon
31	1242	53.5	447	7 ADM33380	Adm33380 Human GCS
32	1242	53.5	447	7 ADV91795	Adv91795 Human GCS
33	1242	53.5	447	8 ADV99716	Adv99716 hg-CSF-L-
34	1240.5	53.4	431	8 ADM50827	Adm50827 Human int
35	1239	53.3	450	2 AAW34505	Aaw34505 Heavy cha
36	1239	53.3	450	2 AAY08755	Aay08755 Human IgG
37	1239	53.3	450	5 ABG31890	Abg31890 Full leng
38	1239	53.3	450	8 ADK18343	Adk18343 Antno ac1
39	1238	53.3	326	8 ADP77155	Adp77155 Anti-VAP-
40	1238	53.3	387	8 ADU66957	Adu66957 Murine pr
41	1238	53.3	409	8 ADQ95440	Adq95440 Fusion pr
42	1238	53.3	409	8 ADQ95441	Adq95441 Fusion pr
43	1238	53.3	447	8 ADQ17121	Adq17121 Humanised
44	1238	53.3	449	7 ADM33378	Adm33378 Human GCS
45	1238	53.3	449	9 ADV91793	Adv91793 Human GCS

ALIGNMENTS

RESULT 1	ADM33853	standard; protein; 436 AA.
ID	ADM33853	
XX	ADM33853;	
AC	ADM33853;	
XX		
DT	03-JUN-2004	(first entry)
XX		
DE	Human HuEPO-L-VFcgamma2 fusion protein.	
XX		
KW	Erythropoietin; EPO; immunoglobulin; IgG;	
KW	fragment crystallisation region; Fc; chronic anaemia; renal disease;	
KW	cancer chemotherapy; rheumatoid arthritis; AIDS;	
KW	myelodysplastic syndrome; (HuEPO)-L-VFcgamma2; human.	
OS	Homo sapiens.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..27
FT	Protein	/note= "Signal peptide"
FT		28..192
FT		/note= "EPO"
FT	Peptide	193..208
FT		/note= "Linker"
FT	Protein	209..436
FT		/note= "IgG2 Fc"
FT		390
FT	Misc-difference	/note= "Wild-type Pro substituted by Ser"
XX		
PN	US2003082749-A1.	
XX		
PD	01-MAY-2003.	
XX		
PF	17-AUG-2001; 2001US-00932812.	
XX		
PR	17-AUG-2001; 2001US-00932812.	
XX		
PA	(SUNL/) SUN L K.	
PA	(SUNB/) SUN B N C.	
PA	(SUNC/) SUN C R Y.	
XX		
PI	Sun LK, Sun BNC, Sun CRV;	
XX		
DR	WPI; 2003-616080/58.	
XX		
PT	New recombinant human erythropoietin-L-VFc fusion proteins, useful for	

PT treating patients with chronic anemia caused by renal failure, cancer
PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
PT infection.

PS Claim 3; Fig 2A; 14pp; English.

The invention relates to a recombinant human erythropoietin (HuEpo)-L-VFc fusion protein comprising HuEpo, a peptide linker, and a human immunoglobulin G Fc (fragment crystallisation region) variant. Also included is a carbohydrate-derived cell line producing the human erythropoietin-L-VFc fusion protein cited above in its growth medium in excess of 10 microgramme per million cells in a 24-hour period. The HuEpo-L-VFc fusion protein exhibits an enhanced *in vitro* biological activity of at least 2-fold relative to that of recombinant HuEpo on a molar basis. The flexible peptide linker containing about 20 or fewer amino acids is present between HuEpo and the human IgG Fc variant. The IgG Fc contains amino acid mutations to attenuate effector functions. The human IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with Pro31Ser mutation, human IgG4 with Ser282Pro and Leu253Ala mutations, or human IgG1 with Leu234Val, Leu253Ala and Pro31Ser mutations. The recombinant human erythropoietin-L-VFc fusion proteins are useful for treating patients with chronic anaemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV infection, or myelodysplastic syndrome. The increased activity and prolonged presence of the human erythropoietin-L-VFc fusion protein in the serum, as compared to prior art, leads to lower dosages and less frequent injections. Less fluctuations of the drug in serum concentrations means improved safety and tolerability, and less frequent injections result in better patient compliance and quality of life. The present sequence represents the fusion protein HuEpo-L-VFcgamma2.

Sequence 436 AA;
SQ

Query Match	100.0%	Score 2323	DB 7	Length 436
Basic Local Similarity	100.0%	Pred No 6	3e-155	
Matches 436	Conservative 0	Mismatches 0	Indels 0	Gaps 0

[illegible]

RESULT 2
ADR48984
ID ADR48984 standard: protein: 436 AA

ADRA48984;
02-DEC-2004 (first entry)
HuBPo-L-Fc fusion protein.
antihaemic; nephrotoxic; human; HuBPo-L-vFc; erythropoietin; EPO;
anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
Homo sapiens.
Synthetic.
US2004175824-A1.
09-SEP-2004.
21-JAN-2004; 2004US-00761593.
17-AUG-2001; 2001US-00932812.
(SUNL/) SUN L K.
(SUNB/) SUN B N C.
(SUNC/) SUN C R Y.
Sun LK, Sun BNC, Sun CRY;
WPI; 2004-634851/61.
N-PSDB; ADRA48983.
New recombinant HuBPo-L-vFc fusion protein comprises human erythropoietin
(HuBPo), a peptide linker, and a human IgG Fc variant, useful for
treating chronic anemia due to renal diseases, cancer chemotherapy, or
rheumatoid arthritis.
Claim 3; SEQ ID NO 18; 31pp; English.

A recombinant HuBPO-L-vFc fusion protein comprises human erythropoietin (HuBPO), a peptide linker, and a human IgG Fc variant, is new, INDEPENDENT CLAIMS are also included for the following: a chimeric hamster ovary (CHO)-derived cell line producing the HuBPO-L-vFc fusion protein in its growth medium in excess of 10 microg/g per million cells in a 24 hour period; and a method for making a recombinant fusion protein comprising HuBPO, a flexible peptide linker, and a human IgG Fc variant comprising Protein: The peptide linker containing 20 or fewer amino acids is present between HuBPO and the human IgG Fc variant, and comprises two or more amino acids selected from glycine, serine, alanine, and threonine. The human IgG Fc variant comprises a hinge, CH2, and CH3 domains of NO. 18). IgG2 with Pro31Ser mutation comprising 456 amino acids (SEQ ID NO. 18). It also comprises a hinge, CH2, and CH3 domains of human IgG4 with Pro31Ser and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO. 19). It further comprises a hinge, CH2, and CH3 domains of human IgA1 with Leu234Val, Leu235Ala, and Pro31Ser mutations comprising 415 amino acids (SEQ ID NO. 22). The HuBPO-L-vFc fusion protein exhibiting in vitro biological activity similar to or higher than that of rHuBPO on a molar basis. Preferred CHO-Derived cell line: The CHO-derived cell line excess of 30 microg/g per million cells in a 24 hour period. The human IgG Fc variant comprises a hinge, CH2, CH3 domains of human IgG selected from: IgB1 as SEQ ID NO. 27, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, the IgG Fc contains amino acid mutations to attenuate effector functions, a flexible peptide linker containing 20 or fewer amino acids is present between HuBPO and human IgG Fc variant, and the HuBPO-L-vFc fusion protein exhibits in vitro biological activity similar to or higher than that of rHuBPO on a molar basis. Preferred Method: Making a recombinant fusion protein comprising HuBPO, a flexible peptide linker, and a human IgG Fc variant comprising: generating a CHO-derived cell line; growing the cell line where the recombinant protein is expressed in its growth medium in excess of 10 microg/g per million cells in a 24 hour period; and purifying the expressed protein from (b); where the recombinant fusion protein exhibits in vitro biological activity similar to or higher than that of rHuBPO on a molar basis. Antineumic; Nephrotropic. No biological

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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:21 ; Search time 21.333 Seconds

(Without alignments)
1966.430 Million cell updates/sec

Title: US-10-761-593A-18

Perfect score: 2323

Sequence: 1 MGWHECPAMWLLSLSLP.....MEBALNHVYQKSLSPGK 436

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1236	53.2	326	1 G2HU	Ig gamma-2 chain C
2	1148.5	49.4	374	2 S69339	Ig heavy chain V r
3	1138	49.0	255	4 S31866	Ig gamma-1 chain C
4	1137	48.9	330	1 G4HU	Ig gamma-1 chain C
5	1120.5	48.2	327	1 G4HU	Ig gamma-4 chain C
6	1120	48.2	377	2 A23511	Ig gamma-3 chain C
7	1111	47.8	377	2 A60764	Ig gamma-3 chain C
8	1102	47.4	289	1 G3H0W1	Ig gamma-3 heavy C
9	1088	46.8	234	2 PT0207	Ig gamma chain C r
10	994	42.8	193	1 ZUHU	Ig gamma chain C r
11	907	39.0	328	2 I47160	Ig gamma 2b chain
12	907	39.0	328	2 I47159	Ig gamma 2a chain
13	902.5	38.9	192	1 J00173	Ig gamma chain C r
14	900	38.7	277	2 I47162	Ig gamma 4 chain C
15	897.5	38.6	192	1 I84613	Ig gamma chain C r
16	887	38.2	328	2 I47158	Ig gamma 1 chain C
17	885	38.1	328	2 I47161	Ig gamma 3 chain C
18	872.5	37.6	323	1 GHRB	Ig gamma chain C r
19	858.5	37.0	329	1 G2GP	Ig gamma-2 chain C
20	854	36.8	470	2 S22080	Ig heavy chain pre
21	833	35.9	444	2 PC4436	monoclonal antibody
22	832.5	35.8	308	2 C30554	Ig heavy chain C r
23	832.5	35.8	472	2 S31459	Ig gamma-1 chain C
24	832	35.8	326	2 B50017	Ig gamma-1 chain C
25	823	35.4	324	1 G1MS	Ig gamma-1 chain C
26	818	35.2	329	1 G1MSC	Ig gamma-3 chain C
27	809.5	34.8	333	2 P50018	Ig gamma-1 chain C
28	809.5	34.8	333	2 P50018	Ig gamma-2b chain
29	807	34.7	398	1 G3MSM	Ig gamma-3 chain C

30	805.5	34.7	329	2 S00847	Ig gamma-2c chain
31	797.5	34.3	188	1 I46083	erythropoietin pre
32	794	34.2	322	2 P50019	Ig gamma-2a chain
33	788.5	33.9	469	2 S37483	Ig gamma-2a chain
34	786	33.8	327	2 S06611	Ig gamma-2 chain C
35	780.5	33.6	330	1 G2MSA	Ig gamma-2a chain
36	775.5	33.4	399	1 G2MSAM	Ig gamma-2a chain
37	771.5	33.2	192	1 S28148	erythropoietin pre
38	768	33.1	474	1 G2MS11	Ig gamma-2b chain
39	767.5	33.0	335	1 G2MSAB	Ig gamma-2b chain
40	765.5	33.0	194	1 I46401	erythropoietin pre
41	765.5	33.0	446	2 S40295	Ig gamma-2a chain
42	761.5	32.8	190	2 I46578	erythropoietin - p
43	755.5	32.5	405	1 G2MSBM	Ig gamma-2b chain
44	751.5	32.4	192	1 A24902	erythropoietin pre
45	739.5	31.8	475	2 S01321	Ig gamma-2b chain

ALIGNMENTS

RESULT 1

G2HU
Ig gamma-2 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #ext_change 09-Jul-2004

C/Accession: A93906; A92809; A90752; A93132; A02148

R/Elision: J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co

A/Reference number: A93906; PMID:82197621; PMID:6804948

A/Accession: A93906

A/Molecule type: DNA

A/Residues: 1326 <EUL>

A/Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFC; GB:V00554; GB:J00230; NID:93

A/Note: Lys-326 is probably removed posttranslationally

R/Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A/Reference number: A92809; PMID:81007873; PMID:6774012

A/Accession: A92809

A/Molecule type: protein

A/Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>

A/Note: Trp-156 is at or near the complement-binding site

R/Connell, G.B.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A/Title: The amino acid sequences of the three heavy chain constant region domains of a

A/Reference number: A90752; PMID:80001357; PMID:113060

A/Accession: A90752

A/Molecule type: protein

A/Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198

A/Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793

A/Note: this sequence has since been revised

R/Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A/Reference number: A93132; PMID:80114419; PMID:118920

A/Accession: A93132

A/Molecule type: protein

A/Residues: 238-275 <HOR>

A/Cross-references: UNIPARC:UPI0000173794

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidat

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A>Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstien, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A>Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (L) heavy disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F:2085/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.2%; Score 1236; DB 1; Length 326;
Best Local Similarity 99.6%; Pred. No. 3.4e-77;
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 209 ERKCCVCEPCPPAPVAGSVFLFPPPKKDTLMISRTPEVTCVYVDVSHEDPEVQFMYV 268
DB 99 ERKCCVCEPCPPAPVAGSVFLFPPPKKDTLMISRTPEVTCVYVDVSHEDPEVQFMYV 158
QY 269 DGVEVNAKTKPREEQFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPASIEKTSKT 328
DB 159 DGVEVNAKTKPREEQFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPASIEKTSKT 218
QY 329 KGPQREPOVYTLPPSRREMTKNQVSLTCLVKGFPSYDIAVWESNGQPENNYKTPPMLD 388
DB 219 KGPQREPOVYTLPPSRREMTKNQVSLTCLVKGFPSYDIAVWESNGQPENNYKTPPMLD 278
QY 389 SDGSGFLLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 436
DB 279 SDGSGFLLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 326

RESULT 2

S69339
Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A>Title: Structure of an abnormal heavy chain in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R:Khamlich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 'C', 142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 49.4%; Score 1148.5; DB 2; Length 374;
Best Local Similarity 86.2%; Pred. No. 3.8e-71;
Matches 219; Conservative 8; Mismatches 18; Indels 9; Gaps 3;

QY 192 DSGGGGGGGGSGGSGG-----GSEKRCVVE---CPPCPAP-VAGPSVFLFPPPKKDTLM 242
DB 121 EGYGQGYRPHSGGQGLVTVSSSEPKSCDTHTCPPAPBELLGGSVFLFPPPKKDTLM 180
QY 243 SRTPEVTCVYVDVSHEDPEVQFMYVDGVEVNAKTKPREEQFNSTFRVSVLTIVHODM 302
DB 181 SRTPEVTCVYVDVSHEDPEVQFMYVDGVEVNAKTKPREEQFNSTFRVSVLTIVHODM 240
QY 303 LNKKEYCKVSNKGLPASIEKTSKTGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFY 362
DB 241 LNKKEYCKVSNKGLPASIEKTSKTGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFY 300
QY 363 PSDIAVWESNGQPENNYKTPPMLDSDGFFLYSKLTVDKSRWQGNVFCVSMHEALH 422
DB 301 PSDIAVWESNGQPENNYKTPPMLDSDGFFLYSKLTVDKSRWQGNVFCVSMHEALH 360
QY 423 NHYTKSLSPGK 436
DB 361 NHYTKSLSPGK 374

RESULT 3

S31866
Ig gamma-1 chain C region - synthetic

C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipala, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-253 <FIL>
A:Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PIR
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-253/Region: human Ig gamma-1 chain C region

Query Match 49.0%; Score 1138; DB 4; Length 255;
Best Local Similarity 90.9%; Pred. No. 1.3e-70;
Matches 211; Conservative 9; Mismatches 8; Indels 4; Gaps 2;

QY 209 ERKCCVCEPCPPAP-VAGPSVFLFPPPKKDTLMISRTPEVTCVYVDVSHEDPEVQF 264
DB 24 ESKSCDKHTICPCPPAPBELLGGSVFLFPPPKKDTLMISRTPEVTCVYVDVSHEDPEVQF 83
QY 265 NWYVDGVEVNAKTKPREEQFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPASIEKTSKT 324
DB 84 NWYVDGVEVNAKTKPREEQFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPASIEKTSKT 143
QY 325 ISKTKGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSYDIAVWESNGQPENNYKTPP 384
DB 144 ISKTKGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSYDIAVWESNGQPENNYKTPP 203
QY 385 PMLDSDGFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 436
DB 204 PMLDSDGFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 255

RESULT 4

GHHU
Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Beysnon, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:16 ; Search time 194.667 Seconds

(without alignments)
1580.190 Million cell updates/sec

Title: US-10-761-593A-18

Perfect score: 2323

Sequence: 1 MGVECPAMLMLLSLSLP.....MHEALNHVYQKSLSPGK 436

Scoring table: BLOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_05.80.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1236	53.2	326	1	IGHG2_HUMAN
2	1236	53.2	417	2	OGN093_HUMAN
3	1233	53.1	464	2	OGMZU6_HUMAN
4	1231	53.0	465	2	OGP6C4_HUMAN
5	1222	52.6	470	2	OG8CNA_HUMAN
6	1146.5	49.4	487	2	OG5ZL2_MURJ
7	1144	49.2	679	2	OG6PQ8_HUMAN
8	1143	49.2	348	2	OGPYX1_HUMAN
9	1143	49.2	473	2	OGMZV7_HUMAN
10	1143	49.2	478	2	OGP181_HUMAN
11	1143	49.2	480	2	OGPJFI_HUMAN
12	1137	48.9	330	1	IGHG1_HUMAN
13	1137	48.9	465	2	OG6MK6_HUMAN
14	1137	48.9	466	2	OG1N78_HUMAN
15	1137	48.9	469	2	OG59F4_HUMAN
16	1137	48.9	460	2	OG72P5_HUMAN
17	1137	48.9	470	2	OG725W1_HUMAN
18	1137	48.9	470	2	OGPJU4_HUMAN
19	1137	48.9	472	2	OGN089_HUMAN
20	1137	48.9	475	2	OGSEF5_HUMAN
21	1137	48.9	475	2	OGGMW7_HUMAN
22	1137	48.9	476	2	OG6MX1_HUMAN
23	1133	48.8	473	2	OGP055_HUMAN
24	1133	48.8	475	2	OGMZQ6_HUMAN
25	1133	48.8	480	2	OGN094_HUMAN
26	1133	48.8	481	2	OGN097_HUMAN
27	1133	48.8	482	2	OG72351_HUMAN
28	1130	48.6	466	2	OGMZK6_HUMAN
29	1126.5	48.5	476	2	OGMZK7_HUMAN
30	1126	48.5	475	2	OGN095_HUMAN
31	1126	48.5	544	2	OGPJ95_HUMAN

32	1123	48.3	521	2	OGN4Y9_HUMAN	OGN4Y9_homo sapien
33	1120.5	48.2	327	1	IGHG4_HUMAN	P01861_homo sapien
34	1120.5	48.2	473	2	OGTC63_HUMAN	OGTC63_homo sapien
35	1120	48.2	354	2	OG8TT2_HUMAN	OG8TT2_homo sapien
36	1120	48.2	518	2	OGN030_HUMAN	OGN030_homo sapien
37	1120	48.2	519	2	OG5BM2_HUMAN	OG5BM2_homo sapien
38	1117	48.1	475	2	OG5RE17_PONY	OG5RE17_pongo pygma
39	1112	47.9	509	2	OGNFI7_HUMAN	OGNFI7_homo sapien
40	1107	47.7	290	1	IGHG3_HUMAN	P01860_homo sapien
41	994	42.8	193	1	EPO_HUMAN	P01588_homo sapien
42	994	42.8	193	2	OG45U2_HUMAN	OG45U2_homo sapien
43	902.5	38.9	192	1	EPO_MACRA	P07865_macaca fasc
44	897.5	38.6	192	1	EPO_MACMU	OG28513_macaca mula
45	872.5	37.6	323	1	GC_FABIT	P01870_oryctolagus

ALIGNMENTS

RESULT 1

ID	IGHG2_HUMAN	STANDARD;	PRT;	326 AA.
AC	P01857			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	IG gamma-2 chain C region.			
CN	Name=IGHG2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE OF 2-326.			
RX	MEDLINE=82197621; PubMed=6804948;			
RA	Ellison J.W., Hood L.E.;			
RT	"Linkage and sequence homology of two human immunoglobulin gamma heavy			
RL	chain constant region genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1984-1986(1982).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE OF 88-115.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=611139; DOI=10.1016/0092-8674(82)90183-0;			
RA	Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;			
RT	"Structure of a gene family.";			
RL	Cell 29:671-679(1982).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE OF 99-177 AND 310-326.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=84235992; PubMed=6329676;			
RA	Krawinkel U., Rabbits T.H.;			
RT	"Comparison of the hinge-coding segments in human immunoglobulin gamma			
RL	heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass			
RL	genes.";			
RL	EMBO J. 1:403-407(1982).			
RN	[4]			
RP	PROTEIN SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).			
RX	MEDLINE=81007873; PubMed=674012;			
RA	Wang A.-C., Tung E., Pudenberg H.H.;			
RT	"The primary structure of a human IgG2 heavy chain: genetic,			
RL	evolutionary, and functional implications.";			
RL	J. Immunol. 125:1048-1054(1980).			
RN	[5]			
RP	PROTEIN SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).			
RX	MEDLINE=80001357; PubMed=113060;			
RA	Connell G.E., Parr D.M., Hofmann T.;			
RT	"The amino acid sequences of the three heavy chain constant region			
RL	domains of a human IgG2 myeloma protein.";			
RL	Can. J. Biochem. 57:758-767(1979).			
RN	[6]			
RP	PROTEIN SEQUENCE OF 238-275 (ZIE).			

RX MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;
 RA Hofmann T., Part D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN (7)
 RP SEQUENCE REVISION TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Part D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RA (8)
 RP PROTEIN SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95265298; PubMed=7737190;
 RA Stoppani M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN (9)
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN (10)
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: J00230; AAB59393.1; -, Genomic_DNA.
 DR PIR: A93806; G2HU.
 DR HSSP: P01859; 1-326.
 DR SMR: P01859; 1-326.
 DR HGNC: HGNC:5526; IG_HG2.
 DR MIM: 147110; -.
 DR GO: GO:0003624; C:membrane fraction; NAS.
 DR GO: GO:0003623; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG_C1.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF07654; C1-set; 3.
 DR SMART: SM00407; IG1; 2.
 DR SMART: SM00835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Direct protein sequencing; Immunoglobulin C region;
 KW Immunoglobulin domain.
 FT REGION 1 98
 FT REGION 99 110
 FT REGION 111 219
 FT REGION 220 326
 FT SITE 156 156
 FT DISULFID 14 14
 FT DISULFID 27 83
 FT DISULFID 102 102
 FT DISULFID 103 103
 FT DISULFID 106 106
 FT DISULFID 109 109
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT VARIANT 60 60
 FT NON TER 1
 FT CONFLICT 109 109
 FT NON TER 1
 SQ SEQUENCE 326 AA; 35885 MW; 831087866878CF9C CRC64;
 Query Match 53.2%; Score 1236; DB 1; Length 326;
 S -> A (in myeloma proteins TIL and ZIE).
 /PRTD=VAR 003889.
 C -> S (in Ref. 3).

Best Local Similarity 99.6%; Pred. No. 5.5e-84;
 Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 209 ERKCVCEPCPCAPPAGSVFLFPKPKDITMISTPEVTCVVVDVSHEDPEVQFNWYV 268
 DB 99 ERKCVCEPCPCAPPAGSVFLFPKPKDITMISTPEVTCVVVDVSHEDPEVQFNWYV 158
 QY 269 DGVEVNAKTKPREDFNSTFRVSVLTIVHODMLNGKSKYCKVSKGLPAPLEKTIISKT 328
 DB 159 DGVEVNAKTKPREDFNSTFRVSVLTIVHODMLNGKSKYCKVSKGLPAPLEKTIISKT 218
 QY 329 KQGPPEQVYTLPPSEEMTKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTPPMD 388
 DB 219 KQGPPEQVYTLPPSEEMTKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTPPMD 278
 QY 389 SDGSFPLYSKLTVDKSRMOQGVFSCVMEALAHNHYTKSLSLSPGK 436
 DB 279 SDGSFPLYSKLTVDKSRMOQGVFSCVMEALAHNHYTKSLSLSPGK 326
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 ID Q6N093 HUMAN PRELIMINARY; PRT; 417 AA.
 AC Q6N093;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686I04196 (Fragment).
 GN Name=DKFZp686I04196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Human esophagus tumor;
 RG The German Human CDNA Consortium;
 RA Wamburt R., Haubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fedo G., Han M., Wiemann S., the EMBL/GenBank/DBD databases.
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBD databases.
 DR EMBL: BK640623; CAB5777.1; -, mRNA.
 DR HSSP: P01861; IAD0.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_LIKE.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-set; 3.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG1; 3.
 DR SMART: SM00835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 1
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 Query Match 53.2%; Score 1236; DB 2; Length 417;
 Best Local Similarity 99.6%; Pred. No. 7.6e-84;
 Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 190 ERKCVCEPCPCAPPAGSVFLFPKPKDITMISTPEVTCVVVDVSHEDPEVQFNWYV 249
 QY 269 DGVEVNAKTKPREDFNSTFRVSVLTIVHODMLNGKSKYCKVSKGLPAPLEKTIISKT 328
 DB 250 DGVEVNAKTKPREDFNSTFRVSVLTIVHODMLNGKSKYCKVSKGLPAPLEKTIISKT 309
 QY 329 KQGPPEQVYTLPPSEEMTKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTPPMD 388
 DB 310 KQGPPEQVYTLPPSEEMTKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTPPMD 369

QY	1	MGVHECPAMWLMLLSLSLSPGLCPVLGAPPRLLCSRVLYERYLLTEKKEKENITTCGAHC	60
Db	1	MGVHECPAMWLMLLSLSLSPGLCPVLGAPPRLLCSRVLYERYLLTEKKEKENITTCGAHC	60
QY	61	SLNENIITVPDTKYNFYAMKRMKEVGOQAVEMWOGIALLSAVALGOALLVNSQPWEPBLOL	120
Db	61	SLNENIITVPDTKYNFYAMKRMKEVGOQAVEMWOGIALLSAVALGOALLVNSQPWEPBLOL	120
QY	121	HYDKAVSGLRSLTTLRLGAQKEAISPDDAASAALRLTITATPFRLLPFVYSNFIKGL	180
Db	121	HYDKAVSGLRSLTTLRLGAQKEAISPDDAASAALRLTITATPFRLLPFVYSNFIKGL	180
QY	181	KLYTBACRGTGGSGGGSGGGSGGGSGGSRKCCVECPCPAPVAGBSVFLPPKPKDYL	240
Db	181	KLYTBACRGTGGSGGGSGGGSGGGSGGGSGGSRKCCVECPCPAPVAGBSVFLPPKPKDYL	240
QY	241	MSRTRPEVTCVVYVNDVSHEDPEYQFMYYVNGVYFHNKATKTPREDSFNSTFVVSILTVHQ	300
Db	241	MSRTRPEVTCVVYVNDVSHEDPEYQFMYYVNGVYFHNKATKTPREDSFNSTFVVSILTVHQ	300

QY	361	LYPSNIIAYEMWENSGGPENNYKTT	PMPLDSDGSEFLYSKLTVDKSRNQGVFSCVWHEA	420
Db	361	FYPSIIAYEMWENSGGPENNYKTT <td>PMPLDSDGSEFLYSKLTVDKSRNQGVFSCVWHEA</td> <td>420</td>	PMPLDSDGSEFLYSKLTVDKSRNQGVFSCVWHEA	420
QY	421	LHNHYTOKSLSLSPGK	436	
Db	421	LHNHYTOKSLSLSPGK	436	

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RESULT 2
US-10-761-593A-18
; Sequence 18, Application US/10761593A
; Publication No. US20040175824A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; TITLE OF INVENTION: activities
FILE REFERENCE: 0250N2001-A
CURRENT APPLICATION NUMBER: US/10/761,593A
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 09/932812
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
; SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure
; US-10-761-593A-18

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			Indels	0	Gaps
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Db	1	MGVHCPCAMWLLLSLSLPTGLPYLGAAPRLICSRVLELYLFAKKAENITTCAGHC	60		
Qy	61	SLNEKITVPPKKNFYAMKMEVGOAVYMGALLSEAVLRGALLVNSSQPEEPL	120		
Db	61	SLNEKITVPPKKNFYAMKMEVGOAVYMGALLSEAVLRGALLVNSSQPEEPL	120		
Qy	121	HYDKAVSGLRSLITLLBALGAOKELISPPDASAPPLATTADTPRKLFRYYSNLRKL	180		
Db	121	HYDKAVSGLRSLITLLBALGAOKELISPPDASAPPLATTADTPRKLFRYYSNLRKL	180		
Qy	181	KLTYGCAKRTGDSGGSGSGSGSGSGSGGSGGSGCCVCECPGCPAPVNAGSVFLPPPKKTL	240		
Db	181	KLTYGCAKRTGDSGGSGSGSGSGSGSGGSGGSGGSGKCCVCECPAPVNAGSVFLPPPKKTL	240		
Qy	241	MISRTPEVTCVYVDVSHDEPEVOFNMYVDGVEVHNAKTKPREEOFNSTFRVYSVLTIVHQ	300		
Db	241	MISRTPEVTCVYVDVSHDEPEVOFNMYVDGVEVHNAKTKPREEOFNSTFRVYSVLTIVHQ	300		
Qy	301	DLNKGKVKCKRVNSNGKLPAISIEKTSKTKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKG	360		
Db	301	DLNKGKVKCKRVNSNGKLPAISIEKTSKTKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKG	360		
Qy	361	FYPSDIAEWMBSNGOPENNYYKTPPMLDSDGSFFLYSKLTVYDKSMOOGNVSFCSVMHEA	420		
Db	361	FYPSDIAEWMBSNGOPENNYYKTPPMLDSDGSFFLYSKLTVYDKSMOOGNVSFCSVMHEA	420		
Qy	421	LHNHYTKSLSPGK	436		
Db	421	LHNHYTKSLSPGK	436		

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RESULT 3
US-11-016-518A-18
; Sequence 18, Application US/11016518A
; Publication No. US20050124045A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
TITLE OF INVENTION: biological activities
FILE REFERENCE: 02SUN2004D1
CURRENT APPLICATION NUMBER: US/11/016,518A
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: HUEPO-L-VFC gamma2 with a 27-amino acid leader peptide (Figure
US-11-016-518A-18

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Query Match	Similarity	100.0%	Score 2123	DB 6	Length 436
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					Gaps 0
QY	1	MGVHECAPMTLLSLSTPLGLVLDGAPRLICDSRVLEKYLEAEENITGCAHC	60		
DB	1	MGVHECAPMTLLSLSTPLGLVLDGAPRLICDSRVLEKYLEAEENITGCAHC	60		
QY	61	SLNENITVPPKPNFYAMKMEVGOQAVEWOGALSLSEAVLRCQALLVNSQWPELQ	120		
DB	61	SLNENITVPPKPNFYAMKMEVGOQAVEWOGALSLSEAVLRCQALLVNSQWPELQ	120		
QY	121	HYDAVAGSLSTLTLLPALAQOKAISPAPASAAPRTITADPFRLLFRVSNFLGKL	180		
DB	121	HYDAVAGSLSTLTLLPALAQOKAISPAPASAAPRTITADPFRLLFRVSNFLGKL	180		
QY	181	KLTYGEACRTIDSGGGSGGGSGGGSGGSEKCCYECPCPAPVPVAGSVLPFRKPDTL	240		
DB	181	KLTYGEACRTIDSGGGSGGGSGGGSGGSEKCCYECPCPAPVPVAGSVLPFRKPDTL	240		
QY	241	MISRTPEVTCVVDVSHEDPEVQFNMTYDGVENATKTRREDFNSTFRVSVLTLYHQ	300		
DB	241	MISRTPEVTCVVDVSHEDPEVQFNMTYDGVENATKTRREDFNSTFRVSVLTLYHQ	300		
QY	301	DWLNGEKYKCVSNKGLPASTIEKTIISKTKGQPREPOVYTLPPRSEEMTKQVSLTCLYKG	360		
DB	301	DWLNGEKYKCVSNKGLPASTIEKTIISKTKGQPREPOVYTLPPRSEEMTKQVSLTCLYKG	360		
QY	361	FYPEDIAVEMSNQPENNYKTPPMLDSDGSFFLYSKLTYDSKRMQOGVFCSVNHEA	420		
DB	361	FYPEDIAVEMSNQPENNYKTPPMLDSDGSFFLYSKLTYDSKRMQOGVFCSVNHEA	420		
QY	421	LHNHYTKSLSLSPGK 436			
DB	421	LHNHYTKSLSLSPGK 436			
RESULT 4					
US-11-017-185-18					
; Sequence 18, Application US/11017185					
; Publication No. US20050142642A1					
; GENERAL INFORMATION:					
; APPLICANT: Sun, Lee-Hwei K					
; APPLICANT: Sun, Bill N					
; APPLICANT: Sun, Cecily R					
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biolog					
; TITLE OF INVENTION: activities					

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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:17 ; Search time 117.268 Seconds
(without alignments)
1637.343 Million cell updates/sec

Title: US-10-761-593A-20

Sequence: 1 MGWHECPAMWLLSLSLP.....MHEALHNYTKSLSLGK 437

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2321	100.0	437	7	ADM33855 Human HUE
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3	2321	100.0	437	8	ADM47518 Human EPO
4	2321	100.0	437	9	AEA18935 Human ery
5	2321	100.0	437	9	AEA88755 Human ery
6	2220	95.6	435	7	ADM33857 Human HUE
7	2220	95.6	435	8	ADR48988 Human EPO
8	2220	95.6	435	8	ADM47520 Human EPO
9	2220	95.6	435	9	AEA18937 Human ery
10	2220	95.6	435	9	AEA88757 Human ery
11	2212.5	95.3	436	7	ADM33853 Human HUE
12	2212.5	95.3	436	8	ADR48984 Human EPO
13	2212.5	95.3	436	8	ADM47516 Human EPO
14	2212.5	95.3	436	9	AEA18933 Human ery
15	2212.5	95.3	436	9	AEA88753 Human ery
16	2160	93.1	441	9	AE870229 EPO analo
17	2110.5	90.9	428	8	AE870229 EPO analo
18	2110.5	90.9	428	9	AD010513 EPO signa
19	2110.5	90.9	428	9	ADV97050 Human ery
20	2058.5	88.7	420	5	AAE15348 Human ery
21	1961	84.5	425	7	ABU64199 Plaamid P
22	1961	84.5	425	8	AD010511 Kb signal
23	1932.5	83.3	444	9	ADV97042 Human EPO
24	1346.5	58.0	449	7	ADM33378 Human GCS

25	1346.5	58.0	449	9	ADV91793
26	1346.5	58.0	449	9	ADV9714 hg-CSF-L-
27	1345	57.9	433	8	ADM50825 Human Int
28	1322	57.0	433	2	AAW18579 Interfero
29	1301	56.1	432	2	AAW17903 Human IFN
30	1293.5	55.7	284	6	AAE30927 Gly8-Glu2
31	1256.5	54.1	266	8	ADJ52121 CH1 delet
32	1255.5	54.1	326	2	AAW76221 Human che
33	1255.5	54.1	328	2	AAW76220 Human che
34	1251.5	53.9	331	2	AAW76222 Human che
35	1250	53.9	331	2	AAW76223 Human che
36	1245.5	53.7	447	7	ADM33380 Human GCS
37	1245.5	53.7	447	9	ADV91795 Human GCS
38	1245.5	53.7	447	9	ADV9716 hg-CSF-L-
39	1244	53.6	431	8	ADM50827 Human int
40	1243.5	53.6	754	3	AAW11692 Human sec
41	1243.5	53.6	784	3	AAW11694 Human sec
42	1241.5	53.5	403	7	ADD32018 Heterolog
43	1239	53.4	396	2	AAW10535 Leptin 1-
44	1238	53.3	382	2	AAW90922 IL4.Y124D
45	1238	53.3	448	7	ADM33376 Human GCS

ALIGNMENTS

RESULT 1	ADM33855	ADM33855 standard; protein; 437 AA.
XX	AC	ADM33855;
XX	DT	03-JUN-2004 (first entry)
XX	DE	Human HUEPO-L-VFegamma4 fusion protein.
XX	KW	Erythropoietin; EPO; immunoglobulin; IgG; fragment crystallisation region; Fc; chronic anaemia; renal disease;
KW	KM	cancer chemotherapy; rheumatoid arthritis; AIDS; myelodysplastic syndrome; (HUEPO)-L-VFegamma4; human.
XX	OS	Homo sapiens.
OS	OS	Synthetic.
XX	Key	Location/Qualifiers
FT	Peptide	1..27 /note= "Signal peptide"
FT	Protein	28..192 /note= "EPO"
FT	Peptide	193..208 /note= "linker"
FT	Protein	209..437 /note= "IgG4 Fc"
FT	Misc-difference	219 /note= "Wild-type Ser substituted by Pro"
FT	Misc-difference	226 /note= "Wild-type Leu substituted by Ala"
FT	US2003082749-A1.	
XX	PN	01-MAY-2003.
XX	PD	17-AUG-2001; 2001US-00932812.
XX	PR	17-AUG-2001; 2001US-00932812.
XX	PA	(SUNL/) SUN L K.
PA	PA	(SUNB/) SUN B N C.
PA	PA	(SUNC/) SUN C R Y.
XX	PI	Sun LK, Sun BNC, Sun CRY;
XX	DR	WPI; 2003-616080/58.

DR N-PSDB; ADM33854.

XX New recombinant human erythropoietin-L-vFc fusion proteins, useful for
 PT treating patients with chronic anemia caused by renal failure, cancer
 PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
 PT infection.

PS Claim 4; Fig 2B; 14pp; English.

XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
 CC fusion protein comprising HuBPO, a peptide linker, and a human
 CC immunoglobulin G Fc (fragment crystallisation region) variant. Also
 CC included is a carbohydrate-derived cell line producing the human
 CC erythropoietin-L-vFc fusion protein cited above in its growth medium in
 CC excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
 CC -L-vFc fusion protein exhibits an enhanced in vitro biological activity
 CC of at least 2-fold relative to that of recombinant HuEPO on a molar
 CC basis. The flexible peptide linker containing about 20 or fewer amino
 CC acids is present between HuBPO and the human IgG Fc variant. The IgG Fc
 CC containing amino acid mutations to attenuate effector functions. The human
 CC IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
 CC Pro31Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
 CC human IgG1 with Leu234Val, Leu235Ala and Pro31Ser mutations. The
 CC recombinant human erythropoietin-L-vFc fusion proteins are useful for
 CC treating patients with chronic anaemia caused by renal failure, cancer
 CC chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
 CC infection, or myelodysplastic syndrome. The increased activity and
 CC prolonged presence of the human erythropoietin-L-vFc fusion protein in
 CC the serum, as compared to prior art, leads to lower dosages and less
 CC frequent injections. Less fluctuations of the drug in serum and less
 CC concentrations means improved safety and tolerability, and less frequent
 CC injections result in better patient compliance and quality of life. The
 CC present sequence represents the fusion protein HuBPO-L-vFcgamma4a4.

SQ Sequence 437 AA:

Query Match 100.0%; Score 2321; DB 7; Length 437;

Best Local Similarity 100.0%; Pred. No. 3,6e-148; Indels 0; Gaps 0;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVEHCAPAMLLIILSLISLPLGLVIGAPRLICDSHVLERYLLAEKAEANTTTGCAHC 60
 DB 1 MGVEHCAPAMLLIILSLISLPLGLVIGAPRLICDSHVLERYLLAEKAEANTTTGCAHC 60
 QY 61 SINENITVPDTKYNFYAMKMEVGOQAVEVWQGLALISEAVLRGQALLVNSSQPWEFLQT 120
 DB 61 SINENITVPDTKYNFYAMKMEVGOQAVEVWQGLALISEAVLRGQALLVNSSQPWEFLQT 120
 QY 121 HVDKAVSGILSLTTLNLRALGAOKRAISPPDAASAPRLITADTFRKLFRVYNSFLRGKL 180
 DB 121 HVDKAVSGILSLTTLNLRALGAOKRAISPPDAASAPRLITADTFRKLFRVYNSFLRGKL 180
 QY 181 KLVTEGACRTGDSGG 240
 DB 181 KLVTEGACRTGDSGG 240
 QY 241 LMTSRFEVTCVVVDVSGQEDPEVQFMNVYGVGEVHNAKTRERBOFGSTRVAVSVLVLH 300
 DB 241 LMTSRFEVTCVVVDVSGQEDPEVQFMNVYGVGEVHNAKTRERBOFGSTRVAVSVLVLH 300
 QY 301 ODVINGEYKCKVSNKGLPSISIEKTSKAGQPREPQVTLTPSOEEMTNQVSLTCLVK 360
 DB 301 ODVINGEYKCKVSNKGLPSISIEKTSKAGQPREPQVTLTPSOEEMTNQVSLTCLVK 360
 QY 361 GFPPSDIAVEMESGQPENNYKTTTPVLDSDGSPFLVSRITLVKSRMOEGNVSCVMHE 420
 DB 361 GFPPSDIAVEMESGQPENNYKTTTPVLDSDGSPFLVSRITLVKSRMOEGNVSCVMHE 420
 QY 421 ALNHNHTQKSLISLIGK 437
 DB 421 ALNHNHTQKSLISLIGK 437

RESULT 2

ID ADR48986 standard; protein; 437 AA.

AC ADR48986;

DT 02-DEC-2004 (first entry)

DE HuEPO-L-vFc fusion protein #1.

XX anti-naemic; nephrotoxic; human; HuBPO-L-vFc; erythropoietin; EPO;

KM anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;

KM AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.

XX Homo sapiens.

OS Synthetic.

PN US2004175824-A1.

XX 09-SEP-2004.

PF 21-JAN-2004; 2004US-00761593.

PR 17-AUG-2001; 2001US-00932812.

XX (SUNB/) SUN L K.

PA (SUNB/) SUN B N C.

PA (SUNC/) SUN C R Y.

XX Sun LK, Sun BMC, Sun CRV;

XX WPI; 2004-634851/61.

DR N-PSDB; ADR48985.

PS Claim 4; SEQ ID NO 20; 31pp; English.

XX A recombinant HuBPO-L-vFc fusion protein comprises human erythropoietin
 CC (HuEPO), a peptide linker, and a human IgG Fc variant, is new.
 CC INDEPENDENT CLAIMS are also included for the following: a Chinese hamster
 CC ovary (CHO)-derived cell line producing the HuBPO-L-vFc fusion protein in
 CC its growth medium in excess of 10 microg per million cells in a 24 hour
 CC period; and a method for making a recombinant fusion protein comprising
 CC HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred
 CC between HuBPO and the human IgG Fc variant, and comprises two or more
 CC amino acids selected from glycine, serine, alanine, and threonine. The
 CC human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human
 CC IgG2 with Pro31Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
 CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
 CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
 CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1
 CC with Leu234Val, Leu235Ala, and Pro31Ser mutations comprising 435 amino
 CC acids (SEQ ID NO. 22). The HuBPO-L-vFc fusion protein exhibits in vitro
 CC biological activity similar to or higher than that of HuEPO on a molar
 CC basis. Preferred CHO-derived cell line: The CHO-derived cell line
 CC producing the HuBPO-L-vFc fusion protein in its growth medium in excess
 CC of 10 microg per million cells in a 24 hour period. The human IgG Fc
 CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from
 CC IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
 CC a flexible peptide linker containing 20 or fewer amino acids is present
 CC between HuBPO and human IgG Fc variant, and the HuBPO-L-vFc fusion
 CC protein exhibits in vitro biological activity similar to or higher than
 CC that of HuEPO on a molar basis. Preferred Method: Making a recombinant
 CC fusion protein comprising HuBPO, a flexible peptide linker, and a human
 CC IgG Fc variant comprising: generating a CHO-derived cell line; growing the
 CC cell line where the recombinant protein is expressed in its growth medium
 CC in excess of 10 microg per million cells in a 24 hour period; and

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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:21 ; Search time 21.3823 Seconds

(without alignments)
1966.430 Million cell updates/sec

Title: US-10-761-593A-20

Perfect score: 2321
Sequence: 1 MGVHECPRAWMLLSLSLSP.....MREALNHYTKSLSLCK 437Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1226	52.8	327	1	G4HU	Ig gamma-4 chain C
2	1144	49.3	374	2	S69339	Ig heavy chain V r
3	1138	49.0	255	4	S31866	Ig gamma-1 chain C
4	1138	49.0	330	1	GHHU	Ig gamma-1 chain C
5	1125.5	48.5	326	1	G2HU	Ig gamma-2 chain C
6	1123	48.4	377	2	A60764	Ig gamma-3 chain C
7	1113	48.0	377	2	A23511	Ig gamma-3 chain C
8	1101	47.4	234	2	PT0207	Ig gamma-1 chain C
9	1095	47.2	289	1	G3HUI	Ig gamma-3 heavy C
10	994	42.8	193	1	ZUHU	erythropoietin pre
11	916.5	39.5	328	2	I47160	Ig gamma 2b chain
12	916.5	39.5	328	2	I47159	Ig gamma 2a chain
13	908.5	39.1	277	2	I47162	Ig gamma 4 chain C
14	902.5	38.9	192	1	JU0173	erythropoietin pre
15	897.5	38.7	192	1	I84613	Ig gamma 3 chain C
16	893.5	38.5	328	2	I47161	Ig gamma 3 chain C
17	882	38.0	323	1	GHRB	Ig gamma chain C r
18	878.5	37.9	328	2	I47158	Ig gamma 1 chain C
19	871.5	37.5	470	2	S22080	Ig heavy chain pre
20	851	36.7	329	1	G2GP	Ig gamma-2 chain C
21	850	36.6	472	2	S31459	Ig gamma-1 chain -
22	848	36.5	308	2	G30554	Ig heavy chain C r
23	819.5	35.3	333	2	PS0018	Ig gamma-2b chain
24	815	35.1	329	1	G3MSC	Ig gamma-3 chain C
25	813.5	35.0	444	2	PC4456	monoclonal antibod
26	810.5	34.9	326	2	PS0017	Ig gamma-1 chain C
27	808	34.8	469	2	S37483	Ig gamma-2a chain
28	807	34.8	398	1	G3MSM	Ig gamma-3 chain C
29	803.5	34.6	324	1	G1MS	Ig gamma-1 chain C

30	802	34.6	329	2	S00847	Ig gamma-2c chain
31	798.5	34.4	330	1	G2MSA	Ig gamma-2a chain
32	798.5	34.4	333	1	G1MSM	Ig gamma-1 chain C
33	798	34.4	335	1	G2MSAB	Ig gamma-2a chain
34	797.5	34.4	188	1	I46083	erythropoietin pre
35	793.5	34.2	399	1	G2MSAM	Ig gamma-2a chain
36	783.5	33.8	446	2	S40295	Ig gamma-2b chain
37	773.5	33.3	474	1	G2MS11	Ig gamma-2b chain
38	771.5	33.2	192	1	S28148	erythropoietin pre
39	767.5	33.1	327	2	S06611	Ig gamma-2 chain C
40	765.5	33.0	194	1	I46401	erythropoietin pre
41	765.5	33.0	405	1	G2MSBM	Ig gamma-2b chain
42	764	32.9	322	2	PS0019	Ig gamma-2b chain
43	761.5	32.8	190	2	I46578	erythropoietin pre
44	751.5	32.4	192	1	A24902	erythropoietin pre
45	743.5	32.0	475	2	S01321	Ig gamma-2b chain

ALIGNMENTS

RESULT 1

G4HU
Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence.revision 02-Apr-1982 #ext_change 09-Jul-2004

C/Accession: A90933; A90249; A02150

R/Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Accession: A90933; MWID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1327 <ELL>

A/Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A/Note: The sequence was determined from the germline gene

R/Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A/Reference number: A90249; MWID:70207560; PMID:4192659

A/Accession: A90249

A/Molecule type: protein

A/Residues: 130;81-326 <PIN>

A/Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Intons: 99/1; 111/1; 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.

C/Superfamily: Immunoglobulin C region; Immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology <IM1>

F/99-110/Region: hinge

F/134-203/Domain: immunoglobulin homology <IM2>

F/240-307/Domain: immunoglobulin homology <IM3>

F/14/Disulfide bonds: interchain (to light chain) #status experimental

F/27-83,141-201,247-305/Disulfide bonds: #status predicted

F/106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F/177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.8%; Score 1226; DB 1; Length 327;

Best Local Similarity 99.1%; Pred. No. 3.4e-74; Mismatches 2; Indels 0; Gaps 0;

Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	209	ESKKGPPCPCPAPAFAGGVSFLFPKPKDITMISRTSEVTCVVVDVSGEDPEVQFNWY	268
DB	99	ESKKGPPCPCPAPAFAGGVSFLFPKPKDITMISRTSEVTCVVVDVSGEDPEVQFNWY	158
QY	269	VDGVEVHNATKPREQFNSTYRVSVLVTVLHODMNGKRYKCKVSNKGLPSSIEKTIK	328
DB	159	VDGVEVHNATKPREQFNSTYRVSVLVTVLHODMNGKRYKCKVSNKGLPSSIEKTIK	218

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:16 ; Search time 195.113 Seconds

(without alignments)
1580.190 Million cell updates/sec

Title: US-10-761-593a-20

Perfect score: 2321

Sequence: 1 MGVHECPALWLLSLSLP.....MHKALHNYTKSLSLGK 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_05.80:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1226	52.8	337	1	IGHG4_HUMAN	P01861 homo sapien
2	1226	52.8	473	1	IGHG6_HUMAN	O81C63 homo sapien
3	1220	52.6	476	2	Q6MZX7_HUMAN	Q6MZX7 homo sapien
4	1152	49.6	487	2	Q65ZL2_MOUSE	Q65ZL2 mus sp. f/v
5	1144	49.3	348	2	Q6PYX1_HUMAN	Q6PYX1 homo sapien
6	1144	49.3	473	2	Q6MZV7_HUMAN	Q6MZV7 homo sapien
7	1144	49.3	478	2	Q6P181_HUMAN	Q6P181 homo sapien
8	1144	49.3	480	2	Q6P181_HUMAN	Q6P181 homo sapien
9	1138	49.0	330	1	IGHG1_HUMAN	P01857 homo sapien
10	1138	49.0	465	2	Q6GMX6_HUMAN	Q6GMX6 homo sapien
11	1138	49.0	466	2	Q6IN78_HUMAN	Q6IN78 homo sapien
12	1138	49.0	469	2	Q659F4_HUMAN	Q659F4 homo sapien
13	1138	49.0	469	2	Q6Z7P5_HUMAN	Q6Z7P5 homo sapien
14	1138	49.0	470	2	Q7Z5W1_HUMAN	Q7Z5W1 homo sapien
15	1138	49.0	470	2	Q6PJ44_HUMAN	Q6PJ44 homo sapien
16	1138	49.0	472	2	Q6N089_HUMAN	Q6N089 homo sapien
17	1138	49.0	475	2	Q5EFES_HUMAN	Q5EFES homo sapien
18	1138	49.0	475	2	Q6GMW7_HUMAN	Q6GMW7 homo sapien
19	1138	49.0	475	2	Q6GMX1_HUMAN	Q6GMX1 homo sapien
20	1138	49.0	679	2	Q96F08_HUMAN	Q96F08 homo sapien
21	1134	48.9	473	2	Q6P055_HUMAN	Q6P055 homo sapien
22	1134	48.9	475	2	Q6MZ06_HUMAN	Q6MZ06 homo sapien
23	1134	48.9	480	2	Q6N094_HUMAN	Q6N094 homo sapien
24	1134	48.9	481	2	Q6N097_HUMAN	Q6N097 homo sapien
25	1134	48.9	482	2	Q7Z351_HUMAN	Q7Z351 homo sapien
26	1131	48.7	466	2	Q6N096_HUMAN	Q6N096 homo sapien
27	1130	48.7	544	2	Q6PJ35_HUMAN	Q6PJ35 homo sapien
28	1127	48.6	475	2	Q6N095_HUMAN	Q6N095 homo sapien
29	1125.5	48.5	326	1	IGHG2_HUMAN	P01859 homo sapien
30	1125.5	48.5	417	2	Q6N093_HUMAN	Q6N093 homo sapien
31	1122.5	48.4	464	2	Q6MZU6_HUMAN	Q6MZU6 homo sapien

32	1121	48.3	475	2	Q5RE17_PONPY	Q5RE17 pongo pygma
33	1120.5	48.3	465	2	Q6P6C4_HUMAN	Q6P6C4 homo sapien
34	1116	48.1	521	2	Q8N4Y9_HUMAN	Q8N4Y9 homo sapien
35	1113	48.0	354	2	Q86TT2_HUMAN	Q86TT2 homo sapien
36	1113	48.0	518	2	Q6N030_HUMAN	Q6N030 homo sapien
37	1113	48.0	519	2	Q5EBM2_HUMAN	Q5EBM2 homo sapien
38	1111.5	47.9	470	2	Q6ECN4_HUMAN	Q6ECN4 homo sapien
39	1108	47.7	509	2	Q8NFI7_HUMAN	Q8NFI7 homo sapien
40	1100	47.4	290	1	IGHG3_HUMAN	P01860 homo sapien
41	994	42.8	193	2	Q545U2_HUMAN	Q545U2 homo sapien
42	994	42.8	193	2	Q545U2_HUMAN	Q545U2 homo sapien
43	902.5	38.9	192	1	EPO_MACFA	P07865 macaca fasc
44	897.5	38.7	192	1	EPO_MACMU	Q28513 macaca mula
45	882	38.0	323	1	GC_RABIT	P01870 oryctolagus

ALIGNMENTS

```

RESULT 1
ID IGHG4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig gamma-4 chain C region.
GN Name=IGHG4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-16(1981).
RN [2]
RP PROTEIN SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
  constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; K01316; AAB59394.1; ALT_INIT; Genomic_DNA.
CC PIR; A90933; GAHU.
CC PDB; 1ADQ; X-ray; A=118-323.
CC SMR; P01861; 1-327.
CC HGN; HGNC:5528; IGHG4.
CC MIM; 147130; -.
CC GO; GO:0005624; C:membrane fraction; NAS.
CC GO; GO:0003823; F:antigen binding; TAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF07654; C1-set; 3.
CC SMART; SM00407; IgC1; 2.
CC PROSITE; PSS00835; IG_LIKE; 3.
CC PROSITE; PSS00290; IG_MHC; 2.
CC 3D-structure; Direct protein sequencing; Immunoglobulin C region;
  Immunoglobulin domain.
CC REGION 1 98 CH1.
CC REGION 99 110 Hinge.

```

FT REGION 111 220 CH2.
 FT REGION 221 327 CH3.
 FT DISULFID 14 Interchain (with a light chain).
 FT DISULFID 27 83 Interchain (with a heavy chain).
 FT DISULFID 106 106 Interchain (with a heavy chain).
 FT DISULFID 109 109 Interchain (with a heavy chain).
 FT DISULFID 141 201
 FT DISULFID 247 305
 FT NON TER 1
 SQ SEQUENCE 327 AA; 35941 MW; 3EBDBD11EF208E7A CRC64;

Query Match 52.8%; Score 1226; DB 1; Length 327;
 Best Local Similarity 99.1%; Pred. No. 4.5e-82;
 Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 209 ESKYGPCCPCPAPEFAGPSVFLFPPKPKDTLMTISRTPEVTCVVVDVSOEDPEVQFNMY 268
 DB 99 ESKYGPCCPCPAPEFAGPSVFLFPPKPKDTLMTISRTPEVTCVVVDVSOEDPEVQFNMY 158
 QY 269 VDGVEVHNAKTKPREEQFNSTYRVSVLTVLDHQMILGKREYCKCKVSNKGLPSSIEKTIK 328
 DB 159 VDGVEVHNAKTKPREEQFNSTYRVSVLTVLDHQMILGKREYCKCKVSNKGLPSSIEKTIK 218
 QY 329 AKQGPPEPVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPNNTKTPPV 388
 DB 219 AKQGPPEPVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPNNTKTPPV 278
 QY 389 DSDGSFELYSLTVDSKRMQEGNVFSCVMHEALHNHYTQKSLSLSTGK 437
 DB 279 DSDGSFELYSLTVDSKRMQEGNVFSCVMHEALHNHYTQKSLSLSTGK 327

RESULT 2
 Q8T6C3_HUMAN PRELIMINARY; PRT; 473 AA.

AC Q8T6C3; 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHG4 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA MBDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Helel F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
 RA Datchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boesak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Schrein J.R., Jones S.J.M., Marra M.A.,
 RA Schnerbach A., Schrein J.R., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RU Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Straubeberg R.L.,

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025985; AAH25985.1; -, mRNA.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 52.8%; Score 1226; DB 2; Length 473;
 Best Local Similarity 99.1%; Pred. No. 7.4e-82;
 Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 209 ESKYGPCCPCPAPEFAGPSVFLFPPKPKDTLMTISRTPEVTCVVVDVSOEDPEVQFNMY 268
 DB 245 ESKYGPCCPCPAPEFAGPSVFLFPPKPKDTLMTISRTPEVTCVVVDVSOEDPEVQFNMY 304
 QY 269 VDGVEVHNAKTKPREEQFNSTYRVSVLTVLDHQMILGKREYCKCKVSNKGLPSSIEKTIK 328
 DB 305 VDGVEVHNAKTKPREEQFNSTYRVSVLTVLDHQMILGKREYCKCKVSNKGLPSSIEKTIK 364
 QY 329 AKQGPPEPVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPNNTKTPPV 388
 DB 365 AKQGPPEPVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNQGPNNTKTPPV 424
 QY 389 DSDGSFELYSLTVDSKRMQEGNVFSCVMHEALHNHYTQKSLSLSTGK 437
 DB 425 DSDGSFELYSLTVDSKRMQEGNVFSCVMHEALHNHYTQKSLSLSTGK 473

RESULT 3

Q6MZK7_HUMAN PRELIMINARY; PRT; 476 AA.

AC Q6MZK7; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686M24218;
 GN Name=DKFZp686M24218;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human rectum tumor;
 RA The German Human cDNA Consortium;
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640824; CAB45900.1; -, mRNA.
 DR HSSP; P01861; IADQ.
 DR SMR; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 3.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IG1; 3.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.

Page 2

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RESULT 2
US-09-932-812A-22
: Sequence 22, Application US/09932812A
: Patent No. 6900292
: GENERAL INFORMATION:
: APPLICANT: Sun, Lee-Hwei K
: APPLICANT: Sun, Bill N
: APPLICANT: Sun, Cecily R
: TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
: TITLE OF INVENTION: Increased biological
: TITLE OF INVENTION: activities
: FILE REFERENCE: 02SUN2001
: CURRENT APPLICATION NUMBER: US/09/932,812A
: CURRENT FILING DATE: 2001-08-17
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 22
: LENGTH: 435
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: HUEPO-L-vFc gammaal with a 27-amino acid leader peptide
: OTHER INFORMATION: (Figure 2C
: OTHER INFORMATION: )
: US-09-932-812A-22

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[illegible]

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1 RESULT 3
2 US-09-932-812A-18
3 Sequence 18, Application US/09932812A
4 Patent No. 6900292
5 GENERAL INFORMATION:
6 APPLICANT: Sun, Lee-Hwei K
7 APPLICANT: Sun, Bill N
8 APPLICANT: Sun, Cecily R
9 TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
10 TITLE OF INVENTION: increased biological
11 TITLE OF INVENTION: activities
12 FILE REFERENCE: 02SUN2001
13 CURRENT APPLICATION NUMBER: US/09/932,812A
14 CURRENT FILING DATE: 2001-08-17
15 NUMBER OF SEQ ID NOS: 28
16 SOFTWARE: PatentIn version 3.1
17 SEQ ID NO 18
18 LENGTH: 436
19 TYPE: PRT
20 ORGANISM: Artificial Sequence
21 FEATURE:
22 OTHER INFORMATION: HuPEO-L-WFC gamma2 with a 27-amino acid leader peptide
23 OTHER INFORMATION: (Figure 2
24 OTHER INFORMATION: A)
25 US-09-932-812A-18

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[illegible]

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:42:04 ; Search time 42.0963 Seconds

(without alignments)
441.079 Million cell updates/sec

Title: US-10-761-593A-20

Sequence: 1 MGWHECPRAWMLLSTLSLSP.....MHEALNHVTKSLSLGK 437

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Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2110.5	90.9	428	US-11-029-003-24	Sequence 24, Appl
2	1932.5	83.3	444	US-11-029-003-16	Sequence 16, Appl
3	1240	53.4	497	US-11-274-344-17	Sequence 17, Appl
4	1237.5	53.3	917	US-11-144-987-26	Sequence 26, Appl
5	1237.5	53.3	917	US-11-205-935-26	Sequence 26, Appl
6	1234	53.2	434	US-11-204-709-24	Sequence 24, Appl
7	1234	53.2	902	US-11-144-987-8	Sequence 8, Appl
8	1234	53.2	902	US-11-144-987-14	Sequence 14, Appl
9	1234	53.2	902	US-11-205-935-8	Sequence 8, Appl
10	1234	53.2	902	US-11-205-935-14	Sequence 14, Appl
11	1234	53.2	917	US-11-144-987-20	Sequence 20, Appl
12	1234	53.2	917	US-11-205-935-20	Sequence 20, Appl
13	1229.5	53.0	917	US-11-205-935-24	Sequence 24, Appl
14	1229.5	53.0	917	US-11-205-935-24	Sequence 24, Appl
15	1226	52.8	327	US-10-999-866-38	Sequence 38, Appl
16	1226	52.8	327	US-10-988-207-22	Sequence 22, Appl
17	1226	52.8	327	US-10-935-909-26	Sequence 26, Appl
18	1226	52.8	327	US-10-935-005B-69	Sequence 69, Appl
19	1226	52.8	327	US-11-061-821-38	Sequence 38, Appl
20	1226	52.8	327	US-11-102-621-114	Sequence 114, Appl
21	1226	52.8	327	US-11-124-620-4	Sequence 4, Appl
22	1226	52.8	327	US-11-233-683-4	Sequence 4, Appl
23	1226	52.8	328	US-10-988-207-23	Sequence 23, Appl
24	1226	52.8	329	US-11-122-622-100	Sequence 100, Appl
25	1226	52.8	451	US-11-166-906-1	Sequence 1, Appl

26	1226	52.8	626	7	US-11-050-346-19	Sequence 19, Appl
27	1226	52.8	864	7	US-11-050-346-10	Sequence 10, Appl
28	1226	52.8	864	7	US-11-103-077-29	Sequence 29, Appl
29	1226	52.8	902	7	US-11-144-987-6	Sequence 6, Appl
30	1226	52.8	902	7	US-11-144-987-12	Sequence 12, Appl
31	1226	52.8	902	7	US-11-205-935-6	Sequence 6, Appl
32	1226	52.8	902	7	US-11-205-935-12	Sequence 12, Appl
33	1226	52.8	917	7	US-11-144-987-18	Sequence 18, Appl
34	1226	52.8	917	7	US-11-205-935-18	Sequence 18, Appl
35	1223	52.7	337	7	US-11-102-621-116	Sequence 116, Appl
36	1223	52.7	451	7	US-11-102-621-144	Sequence 144, Appl
37	1221	52.6	326	6	US-10-988-207-24	Sequence 24, Appl
38	1220.5	52.6	430	6	US-11-029-003-22	Sequence 22, Appl
39	1220	52.6	451	7	US-11-102-621-142	Sequence 142, Appl
40	1220	52.6	451	7	US-11-102-621-143	Sequence 143, Appl
41	1217	52.4	437	7	US-11-102-621-117	Sequence 117, Appl
42	1217	52.4	451	7	US-11-102-621-145	Sequence 145, Appl
43	1215	52.3	451	7	US-11-102-621-146	Sequence 146, Appl
44	1204.5	51.9	249	6	US-10-935-005B-89	Sequence 89, Appl
45	1201.5	51.8	247	6	US-10-935-005B-87	Sequence 87, Appl

ALIGNMENTS

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RESULT 1
US-11-029-003-24
; Sequence 24, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTTEL, JAMES
; TITLE OF INVENTION: IMMOBILIZED IN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 24
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-11-029-003-24
Query Match 90.9%; Score 2110.5; DB 7; Length 428;
Best Local Similarity 91.8%; Pred. No. 2.2e-156; Indels 9; Gaps 1;
Matches 401; Conservative 9; Mismatches 18;
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DB	121	HVDKAVGSLSTLTLLALAGOKAISPDAASAAPRTTADFRKLFRVYSNFLRGKL	180
QY	181	KLYTGACRTGDSGGSGGGSGGGSGESKYGPPCPAPFAAGPSVFLFPKPKDT	240

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us-10-761-593a-20.rapbn

Page 2

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Db 232 LMTSRPEYTCVVDVSDPEVQFMVYVGVHNAKTPREPOFSTYRVSVLTVLH 291
Qy 301 QDWLNKGEYKCKVSNKLPSSIEKTKSKAGOPREPOVYTLPRSOEMTKOVSLTCLYK 360
Db 292 QDWLNKGEYKCKVSNKLPAPRIEKTISKAGOPREPOVYTLPRSDRLTKOVSLTCLYK 351
Qy 361 GFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLYSLTVDKSRMOEGNVFSCVME 420
Db 352 GFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLYSLTVDKSRMOEGNVFSCVME 411
Qy 421 ALHNYTQKSLSLSLGK 437
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RESULT 2

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US-11-029-003-16
; Sequence 16, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029, 003
; PRIOR FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-029-003-16
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Query Match 83.3%; Score 1932.5; DB 7; Length 444;
Best Local Similarity 82.4%; Pred. No. 1.5e-142;
Matches 379; Conservative 10; Mismatches 24; Indels 47; Gaps 3;

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Qy 7 PAWMLTLLSLPLGLPLV-LGAPRLICDSRVLYLLEAKENITTTGCAEHCISINEN 65
Db 3 PCTLLILIAALATQTRAGSRAPRLICDSRVLYLLEAKENITTTGCAEHCISINEN 62
Qy 66 ITVPDTKYNFYAMKMEVGOAVVWQGLALLSEAVLRGQALLVNSSQPEPQLAHVKA 125
Db 63 ITVPDTKYNFYAMKMEVGOAVVWQGLALLSEAVLRGQALLVNSSQPEPQLAHVKA 122
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Db 123 VSGLRSLTTLRALGAOKEAISPDAASAPLRTITADTERFKLFRVYSNPLRGKLYTG 182
Qy 186 EACRTGSGSGG-----SGGSGSGSGSGSESKYCPPCP 217
Db 183 EACRTGSGSGG-----SGGSGSGSGSGSESKYCPPCP 216
Qy 218 PCPAPPEAGGSGVFLFPKPKDQTLMTSRPEVTCVVDVSDPEVQFMVYVGVHNA 277
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Db 285 KTKPREOPNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPAPRIEKTISKAGOPREPO 344
Qy 338 VYTLPRSOEMTKOVSLTCLYKGFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLY 397
Db 345 VYTLPRSOEMTKOVSLTCLYKGFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLY 404
Qy 398 SRLTYKSRMOEGNVFSCVMEHALHNYTQKSLSLGK 437
Db 405 SKLTVDKSRMOEGNVFSCVMEHALHNYTQKSLSLSPGK 444
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RESULT 3

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US-11-274-344-17
; Sequence 17, Application US/11274344
; Publication No. US20060067920A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Michael
; TITLE OF INVENTION: Chimeric Immunoceptor Useful In Treating Human Cancers
; FILE REFERENCE: 1954-472
; CURRENT APPLICATION NUMBER: US/11/274,344
; PRIOR FILING DATE: 2005-11-16
; PRIOR APPLICATION NUMBER: 60/286,981
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 10/134,645
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-274-344-17
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Query Match 53.4%; Score 1240; DB 7; Length 497;
Best Local Similarity 73.4%; Pred. No. 1.1e-88;
Matches 248; Conservative 15; Mismatches 50; Indels 25; Gaps 5;

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Db 46 KAPLCNGSMWMS-INLTAGVYCAALBSLINVSGCAIEKTQRMVLSGFCPHKVASAGPFSL 104
Qy 161 -TADTERFKLFRVYSNPLRGKLYTGACRTGDSGSGSGSGSGSGSGSGSGSGSGSG 219
Db 105 HVADTKIEVAGFYKDLHLHKLIF-----RGRFNSKYGPCPCPC 145
Qy 220 PAFEPAGSGSVFLFPKPKDQTLMTSRPEVTCVVDVSDPEVQFMVYVGVHNAKT 279
Db 146 PAFEPAGSGSVFLFPKPKDQTLMTSRPEVTCVVDVSDPEVQFMVYVGVHNAKT 205
Qy 280 KPREOPNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTKSKAGOPREPO 339
Db 206 KPREOPNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTKSKAGOPREPO 265
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Db 266 TLPPSOEMTKOVSLTCLYKGFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLYSR 325
Qy 400 LTYDKSRMOEGNVFSCVMEHALHNYTQKSLSLGK 437
Db 326 LTYDKSRMOEGNVFSCVMEHALHNYTQKSLSLSLGK 363
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; Sequence 26, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

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2891.644 Million cell updates/sec

Title: US-10-761-593A-20

Perfect score: 2321
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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6: /cgn2_6/prodata/1/pubppaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2321	100.0	437	3 US-09-932-812-20	Sequence 20, Appl
2	2321	100.0	437	4 US-10-761-593A-20	Sequence 20, Appl
3	2321	100.0	437	6 US-11-016-518A-20	Sequence 20, Appl
4	2321	100.0	437	6 US-11-017-185-20	Sequence 20, Appl
5	2220	95.6	435	3 US-09-932-812-22	Sequence 22, Appl
6	2220	95.6	435	4 US-10-761-593A-22	Sequence 22, Appl
7	2220	95.6	435	6 US-11-016-518A-22	Sequence 22, Appl
8	2220	95.6	435	6 US-11-017-185-22	Sequence 22, Appl
9	2212.5	95.3	436	3 US-09-932-812-18	Sequence 18, Appl
10	2212.5	95.3	436	4 US-10-761-593A-18	Sequence 18, Appl
11	2212.5	95.3	436	6 US-11-016-518A-18	Sequence 18, Appl
12	2212.5	95.3	436	6 US-11-017-185-18	Sequence 18, Appl
13	2210.5	90.9	428	4 US-10-435-608-10	Sequence 10, Appl
14	2210.5	90.9	428	4 US-10-622-108-10	Sequence 10, Appl
15	2110.5	90.9	428	4 US-10-841-250-24	Sequence 24, Appl
16	1961	84.5	425	4 US-10-435-608-8	Sequence 8, Appl
17	1961	84.5	425	4 US-10-622-108-8	Sequence 8, Appl
18	1932.5	83.3	444	5 US-10-841-250-16	Sequence 16, Appl
19	1346.5	58.0	449	5 US-09-968-362-20	Sequence 20, Appl
20	1346.5	58.0	449	5 US-10-800-497-20	Sequence 20, Appl
21	1346.5	58.0	449	5 US-10-433-108-24	Sequence 24, Appl
22	1293.5	55.7	266	4 US-10-609-783B-51	Sequence 51, Appl
23	1256.5	54.1	266	4 US-10-287-035-58	Sequence 58, Appl
24	1252.5	54.0	782	4 US-09-968-362-22	Sequence 22, Appl
25	1245.5	53.7	447	5 US-10-800-497-22	Sequence 22, Appl
26	1245.5	53.7	447	5 US-10-800-497-22	Sequence 22, Appl
27	1245.5	53.7	447	5 US-10-800-449-22	Sequence 22, Appl

28	1244.5	53.6	782	4 US-10-287-035-48	Sequence 48, Appl
29	1239	53.4	396	3 US-09-859-361-5	Sequence 5, Appl
30	1238.5	53.4	778	4 US-10-287-035-56	Sequence 56, Appl
31	1238.5	53.4	778	4 US-10-287-035-60	Sequence 60, Appl
32	1238	53.3	382	4 US-10-050-227-10	Sequence 10, Appl
33	1238	53.3	448	3 US-09-968-362-18	Sequence 18, Appl
34	1238	53.3	448	3 US-10-800-497-18	Sequence 18, Appl
35	1238	53.3	448	5 US-10-800-449-18	Sequence 18, Appl
36	1237.5	53.3	782	4 US-10-287-035-54	Sequence 54, Appl
37	1237.5	53.3	917	4 US-10-282-162-56	Sequence 56, Appl
38	1237.5	53.3	917	5 US-10-840-138-26	Sequence 26, Appl
39	1237.5	53.3	917	5 US-10-945-068-26	Sequence 26, Appl
40	1237.5	53.3	917	6 US-11-056-730-26	Sequence 26, Appl
41	1237.5	53.3	917	6 US-11-134-114-56	Sequence 56, Appl
42	1236	53.3	446	5 US-10-644-277-62	Sequence 62, Appl
43	1235.5	53.2	444	5 US-10-492-228-57	Sequence 57, Appl
44	1235.5	53.2	782	3 US-09-935-868-48	Sequence 48, Appl
45	1235.5	53.2	782	3 US-09-935-868-52	Sequence 52, Appl

ALIGNMENTS

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RESULT 1
US-09-932-812-20
; Sequence 20, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biolo
; FILE REFERENCE: 025UN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuBPO-L-vfc gamma4 with a 27-amino acid leader peptide (Figure 2
; OTHER INFORMATION: )
US-09-932-812-20

Query Match 100.0%; Score 2321; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.1e-153; Indels 0; Gaps 0;
Matches 437; Conservative 0; Mismatches 0;

QY 1 MGVEHCPAMWLMLSLSLSPGLPVIGAPPRLLCDSEVLERYLLEAKENITTCAEHC 60
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Db 1 MGVEHCPAMWLMLSLSLSPGLPVIGAPPRLLCDSEVLERYLLEAKENITTCAEHC 60

QY 61 SLNENITVPPTKYNFYAKKMEVGOQAVEVWQGLLSEAVLRGQALLVNSSQPEPLQL 120
|||||
Db 61 SLNENITVPPTKYNFYAKKMEVGOQAVEVWQGLLSEAVLRGQALLVNSSQPEPLQL 120

QY 121 HVDKAVSGLSLSTTLRALGAKQKALSPPPMAAARLRTTATPFRLLPVSNSPLRGL 180
|||||
Db 121 HVDKAVSGLSLSTTLRALGAKQKALSPPPMAAARLRTTATPFRLLPVSNSPLRGL 180

QY 121 HVDKAVSGLSLSTTLRALGAKQKALSPPPMAAARLRTTATPFRLLPVSNSPLRGL 180
|||||
Db 121 HVDKAVSGLSLSTTLRALGAKQKALSPPPMAAARLRTTATPFRLLPVSNSPLRGL 180

QY 181 KLVYGEACRTGDSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 240
|||||
Db 181 KLVYGEACRTGDSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 240

QY 241 LMTSRTPBVTQVVDVSDPEVQFMNYYVDGVEVHNAKTYRREDFNSYTRVVSVLTVH 300
|||||
Db 241 LMTSRTPBVTQVVDVSDPEVQFMNYYVDGVEVHNAKTYRREDFNSYTRVVSVLTVH 300

QY 301 QDWLNGEYKCYKSNKLPSSIEKTTISKAGQPREPOVYTLPSQSEMTNNOVSLTCLVK 360
|||||
Db 301 QDWLNGEYKCYKSNKLPSSIEKTTISKAGQPREPOVYTLPSQSEMTNNOVSLTCLVK 360

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Tue Apr 18 11:54:45 2006

us-10-761-593a-20.rapbm

Page 2

Qy		361	FPPYPBDIAEWMSGNGCPENNNYKTPPYLBSDSGFPFLYSRLTYPKSRMOEGVFCSTWHE	420
Dd		361	GFPISDIAEWSMSGNGCPENNKKTPPYLBSDSGFFLSRLTVDSKRNOEGNVFCSYWHE	420
Qy		421	ALHNHYTKSLSLCK	437
Dd		421	ALHNHYTKSLSLCK	437

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RESULT 2
US-10-761-593A-20
; Sequence 20, Application US/10761593A
; Publication No. US20040175824A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Billy R
APPLICANT: Sun, Bill N
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
TITLE OF INVENTION: activities
FILE REFERENCE: 02SUN2001-A
CURRENT APPLICATION NUMBER: US/10/761,593A
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 09/932812
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HUEBO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure
US-10-761-593A-20

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Query Match	Similarity	100.0%	Score	2321	DB 4	Length	437
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Db	1	MGVHCEPAMLMILSLISLPLGLPVGAPPRLLICDSVTERLYLAEKAEINTTGCAREHC	60				
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Db	61	SLNENITVPDTKNPFAAKRMEVGOQAVEWQGLALISEAVLRGOALLVNSSQWEPRIQL	120				
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Db	121	HYDKAVSGLRSLTTLTLPALGAQKEBALISPPDASAPLRITTTADTFPKLPRVYSNFKRL	180				
QY	181	KLYTGACRTGDGSGGSGSGGSGGSGGSGSKYGPCCPPCAPAFAGDSVFLFPKPKDT	240				
Db	181	KLYTGACRTGDGSGGSGSGGSGGSGGSGSKYGPCCPPCAPAFAGDSVFLFPKPKDT	240				
QY	241	LMISRTPEVTCVVAVDVSQEDPEVQFMNMYVDGVEVHNAKTKRREDFNSTYRVASVLTVLH	300				
Db	241	LMISRTPEVTCVVAVDVSQEDPEVQFMNMYVDGVEVHNAKTKRREDFNSTYRVASVLTVLH	300				
QY	301	QDLNGKEKVKCKVSNKGLPSSIEKTIISKAKQPRPEPVYTLPSQSEEMTKNQVSLTCLVK	360				
Db	301	QDLNGKEKVKCKVSNKGLPSSIEKTIISKAKQPRPEPVYTLPSQSEEMTKNQVSLTCLVK	360				
QY	361	GFYPSDIAVEMBSNGQPENNYKTTPLVLDSDGSFFLYSRLTVDSKRMQEGNVFSCSVNHE	420				
Db	361	GFYPSDIAVEMBSNGQPENNYKTTPLVLDSDGSFFLYSRLTVDSKRMQEGNVFSCSVNHE	420				
QY	421	ALAHNHYTKSLSLSLGK	437				
Db	421	ALAHNHYTKSLSLSLGK	437				

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RESULT 3
US-11-016-518A-20
: Sequence 20, Application US/11016518A
: Publication No. US20050124045A1
: GENERAL INFORMATION:
: APPLICANT: Sun, Lee-Hwei K
: APPLICANT: Sun, Bill N
: TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
: TITLE OF INVENTION: biological activities
: FILE REFERENCE: 025UN2004D
: CURRENT APPLICATION NUMBER: US/11/016,518A
: CURRENT FILING DATE: 2004-12-17
: PRIOR APPLICATION NUMBER: US 09/932,812
: PRIOR FILING DATE: 2001-08-17
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 20
: LENGTH: 437
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figures
: OTHER INFORMATION: 2B)
US-11-016-518A-20

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Query Match	Similarity	100.0%	Score 2321	DB 6	Length 437
Best Local	Similarity	100.0%	Pred. No. 3	1e-153	
Matches 437	Conservative	0	Mismatches	0	Indels
					Gaps 0
Qy	1	MGVHECPAMTLLSLSTSLPLGLGAPPLICDSRVLEERYLLLEAKAEENITTCGAHC	60		
Db	1	MGVHECPAMTLLSLSTSLPLGLGAPPLICDSRVLEERYLLLEAKAEENITTCGAHC	60		
Qy	61	SLNENITVPDKNFYAMKMEVGOAVEWOGIALISEAVLRGOALLVNSGQPEPIQL	120		
Db	61	SLNENITVPDKNFYAMKMEVGOAVEWOGIALISEAVLRGOALLVNSGQPEPIQL	120		
Qy	121	HYDAVAGSGLSTLTLLAALGAOKAISPDAASAAPRTITADPFRKLFRYSNFLGKL	180		
Db	121	HYDAVAGSGLSTLTLLAALGAOKAISPDAASAAPRTITADPFRKLFRYSNFLGKL	180		
Qy	181	KLTYGEACRTDGGGGSGGGSGGGSGGGSEKTPGPCPCPAPEFAGPSVLEFPKRDY	240		
Db	181	KLTYGEACRTDGGGGSGGGSGGGSGGGSEKTPGPCPCPAPEFAGPSVLEFPKRDY	240		
Qy	241	LMISRTPEVTCVYVDVSGOEDPEPVQPMNYVNGVEYHNAKTKPRQENFSTRVSVLVTH	300		
Db	241	LMISRTPEVTCVYVDVSGOEDPEPVQPMNYVNGVEYHNAKTKPRQENFSTRVSVLVTH	300		
Qy	301	QDMLNGEKRYCKRKNKGLPSSIEKTIISKAKGQPEPVYTLTPRQSEMTKQVSLTLVK	360		
Db	301	QDMLNGEKRYCKRKNKGLPSSIEKTIISKAKGQPEPVYTLTPRQSEMTKQVSLTLVK	360		
Qy	361	GFYPSPDIAVEMESNGQPENNYKTTTPVLDSDGSFFLISRLTVDKSRNOEGNVEGCSVMHE	420		
Db	361	GFYPSPDIAVEMESNGQPENNYKTTTPVLDSDGSFFLISRLTVDKSRNOEGNVEGCSVMHE	420		
Qy	421	ALHNHYTQKSLISLSLGK 437			
Db	421	ALHNHYTQKSLISLSLGK 437			

RESULT 4
 US-11-017-185-20
 ; Sequence 20, Application US/11017185
 ; Publication No. US20050142642A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sun, Lee-Hwei K
 ; APPLICANT: Sun, Bill N
 ; APPLICANT: Sun, Cecily R
 ; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biolog
 ; TITLE OF INVENTION: activities

DR N-PSDB; ADM33856.

XX New recombinant human erythropoietin-L-vFc fusion proteins, useful for
PT treating patients with chronic anemia caused by renal failure, cancer
PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
PT infection.

XX Claim 5; Fig 2C; 14pp; English.

XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
XX fusion protein comprising HuEPO, a peptide linker, and a human
XX immunoglobulin G Fc (fragment crystallisation region) variant. Also
XX included is a carbohydrate-derived cell line producing the human
XX erythropoietin-L-vFc fusion protein cited above in its growth medium in
XX excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
XX -L-vFc fusion protein exhibits an enhanced in vitro biological activity
XX of at least 2-fold relative to that of recombinant HuEPO on a molar
XX basis. The flexible peptide linker containing about 20 or fewer amino
XX acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
XX contains amino acid mutations to attenuate effector functions. The human
XX IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
XX Pro31Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
XX human IgG1 with Leu234Val, Leu235Ala and Pro31Ser mutations. The
XX recombinant human erythropoietin-L-vFc fusion proteins are useful for
XX treating patients with chronic anaemia caused by renal failure, cancer
XX chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
XX infection, or myelodysplastic syndrome. The increased activity and
XX prolonged presence of the human erythropoietin-L-vFc fusion protein in
XX the serum as compared to prior art, leads to lower dosages and less
XX frequent injections. Less fluctuations of the drug in serum
XX concentrations means improved safety and tolerability, and less frequent
XX injections result in better patient compliance and quality of life. The
XX present sequence represents the fusion protein HuEPO-L-vFc-gamma1.

XX Sequence 435 AA;

XX Query Match 100.0%; Score 2312; DB 7; Length 435;
XX Best Local Similarity 100.0%; Pred. No. 66-143;
XX Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVEHCPAMWLLLSLSPVGLPVIGAPRLICDSRVLEKYLEAKENITTCQAHC 60
DB 1 MGVEHCPAMWLLLSLSPVGLPVIGAPRLICDSRVLEKYLEAKENITTCQAHC 60
QY 61 SLNENITVPDPTKVFYAMKMEVGOQAVEWQGIALLSEAVIRGQALLVNSSQPMPELOT 120
DB 61 SLNENITVPDPTKVFYAMKMEVGOQAVEWQGIALLSEAVIRGQALLVNSSQPMPELOT 120
QY 121 HYDKAVSGRLSTLTLLRALGQAKAISPPDAASAPLRTITADTFRKLFRVSNFLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGQAKAISPPDAASAPLRTITADTFRKLFRVSNFLRGKL 180
QY 181 KLVYTGACRTGDSGGSGSGSGSGSDTHTCCPPAPAEVAGSPVLFPPKPDITLM 240
DB 181 KLVYTGACRTGDSGGSGSGSGSGSDTHTCCPPAPAEVAGSPVLFPPKPDITLM 240
QY 241 ISRTPEVTCVVVSHEDPEVKFNMYVDGVEVNAKTKPREEQYNSTYRVASVLTVLHOD 300
DB 241 ISRTPEVTCVVVSHEDPEVKFNMYVDGVEVNAKTKPREEQYNSTYRVASVLTVLHOD 300
QY 301 WLNQGEKCKVSKKALPASIEKITSKAKGQPREQVYTLTPPSDELTQKNQVSLTCVKGK 360
DB 301 WLNQGEKCKVSKKALPASIEKITSKAKGQPREQVYTLTPPSDELTQKNQVSLTCVKGK 360
QY 361 YPSDIAVEMSNQPNENNYKTTTPVLDSDGSPFLYSKLTJYDKSRMOQGNVFSQVMEAL 420
DB 361 YPSDIAVEMSNQPNENNYKTTTPVLDSDGSPFLYSKLTJYDKSRMOQGNVFSQVMEAL 420
QY 421 HNHYYTQKSLSTSGK 435
DB 421 HNHYYTQKSLSTSGK 435

RESULT 2
ID ADR48988 standard; protein; 435 AA.
AC ADR48988;
DT 02-DEC-2004 (first entry)
DE HuEPO-L-vFc fusion protein #2.
KW antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;
KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
OS Homo sapiens.
OS Synthetic.
PN US2004175824-A1.
PD 09-SEP-2004.
PF 21-JAN-2004; 2004US-00761593.
PR 17-AUG-2001; 2001US-00932812.
XX (SUNL/) SUN L K.
XX (SUNB/) SUN B N C.
XX (SUNC/) SUN C R Y.
XX Sun LK, Sun BMC, Sun CRY;
XX WPI; 2004-634851/61.
DR N-PSDB; ADR48987.
PT New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
PT (HuEPO), a peptide linker, and a human IgG Fc variant, useful for
PT treating chronic anemia due to renal diseases, cancer chemotherapy, or
PT rheumatoid arthritis.
PS Claim 5; SEQ ID NO 22; 31pp; English.
XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
XX (HuEPO), a peptide linker, and a human IgG Fc variant, is new.
XX INDEPENDENT CLAIMS are also included for the following: a Chinese hamster
XX ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in
XX its growth medium in excess of 10 microg per million cells in a 24 hour
XX period; and a method for making a recombinant fusion protein comprising
XX HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred
XX protein: The peptide linker containing 20 or fewer amino acids is present
XX between HuEPO and the human IgG Fc variant, and comprises two or more
XX amino acids selected from glycine, serine, alanine, and threonine. The
XX human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human
XX IgG2 with Pro31Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
XX It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
XX Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
XX 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1
XX with Leu234Val, Leu235Ala, and Pro31Ser mutations comprising 435 amino
XX acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro
XX biological activity similar to or higher than that of rHuEPO on a molar
XX basis. Preferred CHO-derived cell line: The CHO-derived cell line
XX producing the HuEPO-L-vFc fusion protein in its growth medium in excess
XX of 30 microg per million cells in a 24 hour period. The human IgG Fc
XX variant comprises a hinge, CH2, CH3 domains of human IgG selected from
XX IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
XX the IgG Fc contains amino acid mutations to attenuate effector functions,
XX a flexible peptide linker containing 20 or fewer amino acids is present
XX between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion
XX protein exhibits in vitro biological activity similar to or higher than
XX that of rHuEPO on a molar basis. Preferred Method: Making a recombinant
XX fusion protein comprising HuEPO, a flexible peptide linker, and a human
XX IgG Fc variant comprising: generating a CHO-derived cell line; growing the
XX cell line where the recombinant protein is expressed in its growth medium
XX in excess of 10 microg per million cells in a 24 hour period; and

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:21 ; Search time 21.2844 Seconds
(without alignments)
1966.430 Million cell updates/sec

Title: US-10-761-593A-22
Perfect score: 2312
Sequence: 1 MGHECPAMWLILSLSLP.....MHKALNHYTOKSLSPGK 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1217	52.6	255	4	S31866
2	1217	52.6	330	1	IGHU
3	1211	52.4	374	2	S69339
4	1164	50.3	234	2	PT0207
5	1141.5	49.4	326	1	G2HU
6	1134	49.0	327	1	G4HU
7	1130	48.9	377	2	A23511
8	1128	48.8	377	2	A60764
9	1105	47.8	289	1	G3HUM
10	994	43.0	193	1	ZHUH
11	902.5	33.0	192	1	UC0173
12	902.5	33.0	328	2	I47160
13	902.5	33.0	328	2	I47159
14	901.5	33.0	323	1	GHRB
15	897.5	36.8	192	1	I84613
16	897	38.8	277	2	I47162
17	887.5	38.4	328	2	I47158
18	886	38.3	329	1	G2GP
19	878.5	38.0	328	2	I47161
20	871.5	37.7	470	2	S22080
21	839	36.3	472	2	S31459
22	837	36.2	308	2	C30554
23	833.5	36.1	329	1	PS0548
24	829.5	35.9	333	2	PS0018
25	824.5	35.7	444	2	PC4436
26	822.5	35.6	398	1	G3MSM
27	815.5	35.3	328	2	PS0017
28	814.5	35.2	324	1	G1MS
29	809.5	35.0	393	1	G1MSM

30	802	34.7	469	2	S37483	Ig gamma-2a chain
31	797.5	34.5	188	1	I46083	erythropoietin pre
32	796.5	34.5	329	2	S00847	Ig gamma-2c chain
33	793	34.3	330	1	G2MSA	Ig gamma-2a chain
34	788	34.1	339	1	G2MSA	Ig gamma-2a chain
35	786	34.0	335	1	G2MSAB	Ig gamma-2a chain
36	782.5	33.8	322	2	PS0019	Ig gamma-2a chain
37	778	33.7	446	2	S40295	Ig gamma-2a chain
38	777.5	33.6	474	1	G2MS11	Ig gamma-2b chain
39	771.5	33.4	192	1	S28148	erythropoietin pre
40	771.5	33.4	327	2	S06611	Ig gamma-2 chain C
41	765.5	33.1	194	1	I46401	erythropoietin pre
42	765	33.1	405	1	G2MSBM	Ig gamma-2b chain
43	761.5	32.9	190	2	I46578	erythropoietin - p
44	751.5	32.5	192	1	A24902	erythropoietin pre
45	751	32.5	475	2	S01321	Ig gamma-2b chain

ALIGNMENTS

RESULT 1
S31866
Ig gamma-1 chain C region - synthetic
C/Speices: synthetic
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C/Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C/Accession: S31866
R/Filipula, D.
submitted to the EMBL Data Library, February 1993
A/Description: Screening method for protein-protein interactions of cloned gene products
A/Reference number: S31866
A/Accession: S31866
A/Molecule type: mRNA
A/Residues: 1-255 <FIL>
A/Cross-references: UNIPARC:UPI00011F41F; EMBL:X70421; NID:G33068; PIDN:CAA9866.1; PII
C/Keywords: immunoglobulin
F/1-22/Region: Escherichia coli outer membrane protein A precursor
F/23-255/Region: human Ig gamma-1 chain C region

Query Match 52.6%; Score 1217; DB 4; Length 255;
Best Local Similarity 98.7%; Pred. No. 1.9e-75;
Matches 224; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	209	DKHTPCPCAPAPVAGSPVFLPPPKDITLMSRPPEVTCVVDVSHEDPEVKFNYYVD	268
DB	29	DKHTPCPCAPAPVAGSPVFLPPPKDITLMSRPPEVTCVVDVSHEDPEVKFNYYVD	88
QY	269	GVEVHNAKTPREBOYNSTRVSVLTVLHQMNGEKYCKVSNKALPAPISIEKTISKAK	328
DB	89	GVEVHNAKTPREBOYNSTRVSVLTVLHQMNGEKYCKVSNKALPAPISIEKTISKAK	148
QY	329	GQPREPOVYTLPSRDELITNOVSLTCLVKGFPSPDIIVWESNGQPENNYKTTPTPLDS	388
DB	149	GQPREPOVYTLPSRDELITNOVSLTCLVKGFPSPDIIVWESNGQPENNYKTTPTPLDS	208
QY	389	DGSEFLYSKLTVDKSRWQGNVSCSVMEHALNHYTOKSLSPGK	435
DB	209	DGSEFLYSKLTVDKSRWQGNVSCSVMEHALNHYTOKSLSPGK	255

RESULT 2

IGHU
Ig gamma-1 chain C region - human
C/Speices: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R/Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10: 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A/Reference number: A93433; MUID:82274238; PMID:6287452
A/Accession: A93433
A/Molecule type: DNA

A:Residues: 1-330 <ELL>
A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370
A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A:Note: Lys-330 is removed after transablation
R:Harrie, L.J
Submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: UNIPARC:UPI000013GCFE; EMBL:Z17370
R:Yakubashin, N.; Ueda, S.; Odata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:681139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113,253-330 <TAK>
A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. VI. Amino acid sequence
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96,'R','98-135 <CUN>
A:Cross-references: UNIPARC:UPI000017378D
A:Note: This sequence has the G1m(3) marker
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. VIII. Amino acid sequence
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-150,'Q','156-165,'Q','167-176,'Q','178-194,'N','196-197,'D','199-238,'E',240,
A:Cross-references: UNIPARC:UPI000017378E
A:Note: This sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponslatingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physikol. Chem. 357, 1571-1504, 1976
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q','36-96,'K','98-115,'Q','117-197,'D','199-238,'D','240,'L','242-268,'E',272
A:Cross-references: UNIPARC:UPI000017378F
A:Note: This sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physikol. Chem. 364, 713-747, 1983
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO1
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KO1, disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R','98-197,'D','199-238,'E',240,'W',242-266,'D',268-271,'D',273-330 <SCH>
A:Cross-references: UNIPARC:UPI0000173790
A:Note: This sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dieker, L.; Schwarz, U.; Reitelsh, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physikol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
A:Genetics:
A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la C:superfamily: immunoglobulin C region; immunoglobulin homology
C:keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
P:20-85/domain: immunoglobulin homology <IM>
P:127-306/domain: immunoglobulin homology <IM2>
P:241-310/domain: immunoglobulin homology <IM3>
P:27-83;144-204;250-308/disulfide bonds: #status experimental
P:109;112/disulfide bonds: interchain (to light chain) #status experimental
P:109;112/disulfide bonds: interchain (to heavy chain) #status experimental
P:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 52.6%; Score 1217; DB 1; Length 330;
Best Local Similarity 98.7%; Pred. No. 2,66-75; Indels 0; Gaps 0;
Matches 224; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

209 DKHTTCCPCAPAVAGSPVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFMYVD 268
104 DKHTTCCPCAPAVAGSPVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFMYVD 163
269 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPASIEKTSKAK 328
164 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPAIEKTSKAK 223
329 GQPEEPQVYTLTPSRDELDTNQVSLTCLVGFPSDIAVWESNGCPENNYKTPPVLD 388
224 GQPEEPQVYTLTPSRDELDTNQVSLTCLVGFPSDIAVWESNGCPENNYKTPPVLD 283

389 DGSPFLYSKLTIVDKSRWQGNVFCSGVMEHALHNHTQSLSPK 435
284 DGSPFLYSKLTIVDKSRWQGNVFCSGVMEHALHNHTQSLSPK 330

RESULT 3
569339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilich, A.A.; Auctoutlet, P.; Preud'homme, J.L.; Cogne, M.
Burr, J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; PMID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R:Khamilich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 52.4%; Score 1211; DB 2; Length 374;
Best Local Similarity 97.8%; Pred. No. 7,76-75; Indels 0; Gaps 0;
Matches 222; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

209 DKHTTCCPCAPAVAGSPVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFMYVD 268
148 DKHTTCCPCAPAVAGSPVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFMYVD 207
269 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPASIEKTSKAK 328
208 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPAIEKTSKAK 267

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:16 ; Search time 194.22 Seconds

(without alignments)
1580.190 Million cell updates/sec

Title: US-10-761-593a-22

Perfect score: 2312

Sequence: 1 MEVHECPALWLLSLSLSP.....MEBALHNYTQKSLSPGK 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1228	53.1	487	2	Q65ZL2_9MURI
2	1218.5	52.7	475	2	Q6GMW7_HUMAN
3	1217	52.6	330	1	IGHG1_HUMAN
4	1217	52.6	465	2	Q6GMX6_HUMAN
5	1217	52.6	466	2	Q6IN78_HUMAN
6	1217	52.6	469	2	Q569F4_HUMAN
7	1217	52.6	469	2	Q727P5_HUMAN
8	1217	52.6	470	2	Q7Z5W1_HUMAN
9	1217	52.6	470	2	Q6FUD4_HUMAN
10	1217	52.6	472	2	Q6N089_HUMAN
11	1217	52.6	475	2	Q5EF85_HUMAN
12	1217	52.6	476	2	Q6GMX1_HUMAN
13	1217	52.6	679	2	Q6P088_HUMAN
14	1213	52.5	473	2	Q6P055_HUMAN
15	1213	52.5	475	2	Q6MZ06_HUMAN
16	1213	52.5	480	2	Q6N094_HUMAN
17	1213	52.5	481	2	Q6N097_HUMAN
18	1213	52.5	482	2	Q7Z351_HUMAN
19	1211	52.4	348	2	Q6PYX1_HUMAN
20	1211	52.4	473	2	Q6MZV7_HUMAN
21	1211	52.4	478	2	Q6P181_HUMAN
22	1211	52.4	480	2	Q6PUP1_HUMAN
23	1210	52.3	466	2	Q6N096_HUMAN
24	1206	52.2	475	2	Q6N095_HUMAN
25	1206	52.2	544	2	Q6P395_HUMAN
26	1156	50.0	475	2	Q5R817_PONPY
27	1141.5	49.4	326	1	IGHG2_HUMAN
28	1141.5	49.4	417	2	Q6N093_HUMAN
29	1138.5	49.2	464	2	Q6MZU6_HUMAN
30	1136.5	49.2	465	2	Q6P6C4_HUMAN
31	1135	49.1	476	2	Q6MZX7_HUMAN

32	1134	49.0	327	1	IGHG4_HUMAN	P01861	homo sapien
33	1134	49.0	473	2	Q8TC63_HUMAN	Q8TC63	homo sapien
34	1130	48.9	354	2	Q86TT2_HUMAN	Q86TT2	homo sapien
35	1130	48.9	518	2	Q6N030_HUMAN	Q6N030	homo sapien
36	1130	48.9	519	2	Q5EBM2_HUMAN	Q5EBM2	homo sapien
37	1127.5	48.8	470	2	Q68CN4_HUMAN	Q68CN4	homo sapien
38	1126	48.7	521	2	Q8N4Y9_HUMAN	Q8N4Y9	homo sapien
39	1115	48.2	509	2	Q8NFI7_HUMAN	Q8NFI7	homo sapien
40	1110	48.0	290	1	IGHG3_HUMAN	P01860	homo sapien
41	994	43.0	193	1	EPO_HUMAN	P01588	homo sapien
42	994	43.0	193	2	Q549U2_HUMAN	Q549U2	homo sapien
43	902.5	39.0	192	1	EPO_MACFA	P07865	macaca fasc
44	901.5	39.0	323	1	GC_RABIT	P01870	oryctolagus
45	897.5	38.8	192	1	EPO_MACMU	Q28513	macaca mula

ALIGNMENTS

RESULT 1

Q65ZL2_9MURI PRELIMINARY; PRT; 487 AA.

AC Q65ZL2;
DT 25-OCT-2004 (TREMBLrel). 28, Created
DT 25-OCT-2004 (TREMBLrel). 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel). 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN- ϵ (tau);
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells."
RL Hum. Antibodies Hybrids 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG C1.
DR InterPro; IPR003598; IG C2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG1; 3.
DR SMART; SM00407; IG1; 2.
DR SMART; SM00408; IG2; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 53.1%; Score 1228; DB 2; Length 487;
Best Local Similarity 52.6%; Pred. No. 3.3e-83;
Matches 272; Conservative 31; Mismatches 92; Indels 122; Gaps 13;

QY	9	WLVLLSLSLPGLPVLAGAPRLICDSRVLEKLEAKENITTCAGHCISLN-ENIT	67
DB	3	WSNVFLFELSVTTG-----VHSQVQLQSPDALVYKQASVKISKASGYT	47
QY	68	VPDYKVNFKVAKMEVGGQAVVWGLA-----LISEAVLRQALLVNSQSPWEPLQLH	121
DB	48	FTTHAHLA---WAKQK-PEQGLE-WIGYISPDNDIKYKFKKATLT-----	90
QY	122	VDKAVS-----GASLTTLRAL-----GAQKEA	145
DB	91	ADSSSTAYWQNLSTSDSAVYFCKRSYTGHWGCGTTLTGSGGGSGGGSGGGSGRIQ	150

QY	1	NGVHECCPAMWLILSLSPGLPVIGAPPRICISRVIERYLLENKEKENITGCAEH	60
Db	1	MGVHECCPAMWLILSLSPGLPVIGAPPRICISRVIERYLLENKEKENITGCAEH	60
QY	61	SINENITVPDTKVFYAMKREVEGQAAVEWQGLALSEAVLRGQALLVNSQPMEBLQ	120
Db	61	SINENITVPDTKVFYAMKREVEGQAAVEWQGLALSEAVLRGQALLVNSQPMEBLQ	120
QY	121	HYDKAVSGLRSTLTLLRALGAQKEAISPEDASAPLRITTDTPFKLLPVYSNPLRGKL	180
Db	121	HYDKAVSGLRSTLTLLRALGAQKEAISPEDASAPLRITTDTPFKLLPVYSNPLRGKL	180
QY	181	KLYTEAGCRIGDGGSGGGSGGGSGGSKTHTCPCPAEVAGGGSVFLFPKPKDITLM	240
Db	181	KLYTEAGCRIGDGGSGGGSGGGSGGSKTHTCPCPAEVAGGGSVFLFPKPKDITLM	240
QY	241	ISRTPEVTCVVVDVSHEDPEVKENMYVVOGVEVHNKTKRREQDYNSTYRVASLTVLHOD	3000
Db	241	ISRTPEVTCVVVDVSHEDPEVKENMYVVOGVEVHNKTKRREQDYNSTYRVASLTVLHOD	3000

Tue Apr 18 11:54:46 2006

us-10-761-593a-22.ra1

Page 2

QY	301	WLNQREYCKCVSNKRLPAIEIKTISAKQOPREPOYTLTPSDELTQNOVSLTCLVKG	360
Db	301	WLNQREYCKCVSNKRLPAIEIKTISAKQOPREPOYTLTPSDELTQNOVSLTCLVKG	360
QY	361	YPSDLAVWESNSGQPENNYKTTTPYLDSGSPFLYKTLVDKRMQGNVFSQVWHEAL	420
Db	361	YPSDLAVWESNSGQPENNYKTTTPYLDSGSPFLYKTLVDKRMQGNVFSQVWHEAL	420
QY	421	HNHYTQKSLSLSPGK	435
Db	421	HNHYTQKSLSLSPGK	435

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RESULT 2
US-09-932-812A-20
; Sequence 20, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bili N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fe fusion proteins of human erythropoietin with
; TITLE OF INVENTION: Increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HUPO-L-vFc gamma4 with a 27-amino acid leader peptide
; OTHER INFORMATION: (Figure 2B
; OTHER INFORMATION: )
; US-09-932-812A-20

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Query Match	Similarity	96.0%	Score 2220	DB 22	Length 437
Best Local	Similarity 95.7%	Pred. No. 3	5e-195		
Matches 418	Conservative 10	Mismatches 7	Indels 2	Gaps 1	
QY	1	MGVCECPA	WLLLSLSLSPLGLPTLGA	PPRLICSRVLERILFAKRAENITGCAHC	60
Db	1	MGVCECPA	WLLLSLSLSPLGLPTLGA	PPRLICSRVLERILFAKRAENITGCAHC	60
QY	61	SINENI	TVPDTKVFNYAMKMEVG	GOAWEVWGGLLSBAVIRGALLVNSSQWPEPIQL	120
Db	61	SINENI	TVPDTKVFNYAMKMEVG	GOAWEVWGGLLSBAVIRGALLVNSSQWPEPIQL	120
QY	121	HVDKAV	SGHRSITTLIRALGA	OKEAISPDDAASAPLRTITADTRFKLFRVYSNFRKL	180
Db	121	HVDKAV	SGHRSITTLIRALGA	OKEAISPDDAASAPLRTITADTRFKLFRVYSNFRKL	180
QY	181	KLYTBA	CACTGGSGGGSGGGSGGSGD	SKTH-ACPPCPA	EVAGSGSVFLFPPKPYDT
Db	181	KLYTBA	CACTGGSGGGSGGGSGGSGD	SKTH-ACPPCPA	EVAGSGSVFLFPPKPYDT
QY	239	IMISTP	EPATCVNVDSHEDPEVK	KNMYVDGVEVNAATKPRPEBOYNS	TYRVASVLTJLH
Db	239	IMISTP	EPATCVNVDSHEDPEVK	KNMYVDGVEVNAATKPRPEBOYNS	TYRVASVLTJLH
QY	299	QDMLNG	KKCVSNKALPAS	IEKTIISRAKQGP	PREPOVYTLTPSPSDELTKNOVSLTCYK
Db	299	QDMLNG	KKCVSNKALPAS	IEKTIISRAKQGP	PREPOVYTLTPSPSDELTKNOVSLTCYK
QY	301	QDMLNG	KKCVSNKALPAS	IEKTIISRAKQGP	PREPOVYTLTPSPSDELTKNOVSLTCYK
Db	301	QDMLNG	KKCVSNKALPAS	IEKTIISRAKQGP	PREPOVYTLTPSPSDELTKNOVSLTCYK
QY	359	GFYPSD	IAVEMWSNQ	OPENNYTTPPVLDSDG	SFFLYSKLTVDKSRMOQGNVSCSNVHE
Db	359	GFYPSD	IAVEMWSNQ	OPENNYTTPPVLDSDG	SFFLYSKLTVDKSRMOQGNVSCSNVHE
QY	419	ALHNHY	TOKSLSLSPGK		
Db	419	ALHNHY	TOKSLSLSPGK		

Db 421 ALHNHYTQKSLSLGLK 437

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RESULT 3
US-09-932-812A-18
; Sequence 18, Application US/09932812A
; Patent No. 690292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: Increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: HUBPO-L-HVC gamma2 with a 27-amino acid leader peptid
; OTHER INFORMATION: (Figure 2
; OTHER INFORMATION: A)
US-09-932-812A-18

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Query Match	95.9%;	Score 2216.5;	DB 2;	Length 436;
Best Local Similarity	95.9%;	Pred. No. 7.3e-195;		
Matches 419; Conservative	9;	Mismatches 6;	Indels 3;	Gaps 2;

QY	MGWHECPAMMLLSTLSLPLGLPYLGA	PPRLICDSRYLEBYLLAEAEENITTCGAHC	60
Db	1	MGWHECPAMMLLSTLSLPLGLPYLGA	PPRLICDSRYLEBYLLAEAEENITTCGAHC 60
QY	SLNENITVDPRTKYNFAMKRMVEVGOAV	EWOGALLSEALRGOALLNNSGOWPELOL	120
Db	61	SLNENITVDPRTKYNFAMKRMVEVGOAV	EWOGALLSEALRGOALLNNSGOWPELOL 120
QY	SLNENITVDPRTKYNFAMKRMVEVGOAV	EWOGALLSEALRGOALLNNSGOWPELOL	120
Db	61	SLNENITVDPRTKYNFAMKRMVEVGOAV	EWOGALLSEALRGOALLNNSGOWPELOL 120
QY	121	HYDKAYSGLRSLTTLIRALGAKEALISPD	ASAAPLTTIADPRLKFLRYSNFLAGKL 160
Db	121	HYDKAYSGLRSLTTLIRALGAKEALISPD	ASAAPLTTIADPRLKFLRYSNFLAGKL 160
QY	181	KLTYGECARTGDGSGGGSGGGSGGGSGD	K--THTCPCBPALRYAGGVSYLEPPRKOT 238
Db	181	KLTYGECARTGDGSGGGSGGGSGGGSGD	K--THTCPCBPALRYAGGVSYLEPPRKOT 238
QY	239	LMISRTPEVTCVAVDVSHEDPEYKFNMY	YDGYEVGNATKREEQYNSTRYVSLTVLH 298
Db	240	LMISRTPEVTCVAVDVSHEDPEYKFNMY	YDGYEVGNATKREEQYNSTRYVSLTVLH 298
QY	299	QDWLNKEKYCKVSNKALPASIEKTI	ISKAKGPREPOUYTLTPGSRDELTKNOUSLTCLVK 358
Db	300	QDWLNKEKYCKVSNKALPASIEKTI	ISKAKGPREPOUYTLTPGSRDEMTKNQUSLTCLVK 358
QY	359	GFYPSDIAVWESNQGPPENNYKTTTPV	LDSDGSFFLYSKLTVDSRWQOGNVFSCSVMHE 418
Db	360	GFYPSDIAVWESNQGPPENNYKTTTPV	LDSDGSFFLYSKLTVDSRWQOGNVFSCSVMHE 418
QY	419	ALHNHYTKSLSLSPGK	435
Db	420	ALHNHYTKSLSLSPGK	436

RESULT 4
US-09-9668-362A-22
; Sequence 22: Application US/099668362A22
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill

GenCore version 5.1.7
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OM protein - protein search, using BW model

Run on: April 17, 2006, 08:40:49 ; Search time 62.8555 Seconds
(without alignments)
2891.644 Million cell updates/sec

Title: US-10-761-593a-22

Perfect score: 2312

Sequence: 1 MGVEHCPAMWMLLSLSLP.....KHEALHNYTKSLSPGK 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2312	100.0	435	3	US-09-932-812-22 Sequence 22, Appl
2	2312	100.0	435	4	US-10-761-593a-22 Sequence 22, Appl
3	2312	100.0	435	6	US-11-016-518a-22 Sequence 22, Appl
4	2312	100.0	435	6	US-11-017-185-22 Sequence 22, Appl
5	2220	96.0	437	3	US-09-932-812-20 Sequence 20, Appl
6	2220	96.0	437	4	US-10-761-593a-20 Sequence 20, Appl
7	2220	96.0	437	6	US-11-016-518a-20 Sequence 20, Appl
8	2220	96.0	437	6	US-11-017-185-20 Sequence 20, Appl
9	2216.5	95.9	436	3	US-09-932-812-18 Sequence 18, Appl
10	2216.5	95.9	436	4	US-10-761-593a-18 Sequence 18, Appl
11	2216.5	95.9	436	6	US-11-016-518a-18 Sequence 18, Appl
12	2216.5	95.9	436	6	US-11-017-185-18 Sequence 18, Appl
13	2197.5	95.0	428	4	US-10-435-608-10 Sequence 10, Appl
14	2197.5	95.0	428	4	US-10-622-108-10 Sequence 10, Appl
15	2197.5	95.0	428	5	US-10-841-250-24 Sequence 24, Appl
16	2048	88.6	425	4	US-10-435-608-8 Sequence 8, Appl
17	2048	88.6	425	4	US-10-622-108-8 Sequence 8, Appl
18	1983.5	85.8	444	5	US-10-841-250-16 Sequence 16, Appl
19	1337.5	57.9	447	3	US-09-968-362-22 Sequence 22, Appl
20	1337.5	57.9	447	5	US-10-800-497-22 Sequence 22, Appl
21	1337.5	57.9	447	5	US-10-800-449-22 Sequence 22, Appl
22	1308.5	56.6	430	5	US-10-841-250-22 Sequence 22, Appl
23	1307	56.5	358	6	US-11-045-022-2 Sequence 2, Appl
24	1297.5	56.1	377	6	US-11-045-022-4 Sequence 4, Appl
25	1281	55.4	294	4	US-10-433-108-26 Sequence 26, Appl
26	1281	55.4	302	4	US-10-433-108-25 Sequence 25, Appl
27	1276	55.2	287	4	US-10-433-108-23 Sequence 23, Appl

28	1276	55.2	287	4	US-10-433-108-28 Sequence 28, Appl
29	1276	55.2	287	4	US-10-433-108-31 Sequence 31, Appl
30	1268.5	54.9	269	4	US-10-609-217-10 Sequence 10, Appl
31	1268.5	54.9	269	4	US-10-632-388-10 Sequence 10, Appl
32	1268.5	54.9	269	4	US-10-651-723-10 Sequence 10, Appl
33	1268.5	54.9	269	4	US-10-645-761-10 Sequence 10, Appl
34	1268.5	54.9	269	4	US-10-666-696-10 Sequence 10, Appl
35	1268.5	54.9	269	4	US-10-653-048-10 Sequence 10, Appl
36	1268.5	54.9	269	5	US-10-645-784-10 Sequence 10, Appl
37	1265.5	54.7	277	4	US-10-609-217-20 Sequence 20, Appl
38	1265.5	54.7	277	4	US-10-632-388-20 Sequence 20, Appl
39	1265.5	54.7	277	4	US-10-651-723-20 Sequence 20, Appl
40	1265.5	54.7	277	4	US-10-645-761-20 Sequence 20, Appl
41	1265.5	54.7	277	4	US-10-666-696-20 Sequence 20, Appl
42	1265.5	54.7	277	4	US-10-653-048-20 Sequence 20, Appl
43	1265.5	54.7	277	5	US-10-645-784-20 Sequence 20, Appl
44	1265	54.7	347	4	US-10-272-899a-108 Sequence 108, Appl
45	1264	54.7	250	4	US-10-609-217-1070 Sequence 1070, Appl

ALIGNMENTS

RESULT 1

US-09-932-812-22

Sequence 22, Application US/09932812

Publication No. US20030082749A1

GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill N

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biologic

FILE REFERENCE: 025UN2001

CURRENT APPLICATION NUMBER: US/09/932,812

CURRENT FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 22

LENGTH: 435

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: HUEBO-L-vfc gamma1 with a 27-amino acid leader peptide (figure 2

US-09-932-812-22

Query Match

Best Local Similarity 100.0%; Score 2312; DB 3; Length 435;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGVEHCPAMWMLLSLSLPGLPVLGAPPRILCDSEVLERVLLAKAEKNTTGGAEHC	60
DB	1	MGVEHCPAMWMLLSLSLPGLPVLGAPPRILCDSEVLERVLLAKAEKNTTGGAEHC	60
QY	61	SLNENITVPTKVFYAMKREVGQAWEVQGLALSEAVLRGQALLVNSQPMPELQ	120
DB	61	SLNENITVPTKVFYAMKREVGQAWEVQGLALSEAVLRGQALLVNSQPMPELQ	120
QY	121	HYDKAVSGRLSTTLRLAIGQKEAISPDAASAALRTTADTFPKLFRVYNSPFRGKL	180
DB	121	HYDKAVSGRLSTTLRLAIGQKEAISPDAASAALRTTADTFPKLFRVYNSPFRGKL	180
QY	181	KLYTGACRTGDSGGSGGSGGSGGSDKTHCPCPAPAEVAGPSVFLFPKPDITLM	240
DB	181	KLYTGACRTGDSGGSGGSGGSGGSDKTHCPCPAPAEVAGPSVFLFPKPDITLM	240
QY	241	ISRTPEVTCVVDVSHDEPEVKFNWYDVEVHNATKCPREBOYNSTRVSVLTVLHOD	300
DB	241	ISRTPEVTCVVDVSHDEPEVKFNWYDVEVHNATKCPREBOYNSTRVSVLTVLHOD	300
QY	301	WLNKGYKCKVSKKALPASIEKTIKSAKQPRPQVYTLPPSDELTKQOVSLTCLVKGF	360
DB	301	WLNKGYKCKVSKKALPASIEKTIKSAKQPRPQVYTLPPSDELTKQOVSLTCLVKGF	360

QY 361 YPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEAL 420
DB 361 YPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEAL 420
QY 421 HNHYYTQKSLSLSPGK 435
DB 421 HNHYYTQKSLSLSPGK 435

RESULT 2
US-10-761-593A-22
; Sequence 22, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuBPO-L-vfc gamma1 with a 27-amino acid leader peptide (Figure
; OTHER INFORMATION: 2C)
US-10-761-593A-22

Query Match 100.0%; Score 2312; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 2e-153;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGVHECPAMLWLLSLSLPLGLPVLGAPPRLICDSRVLYERYLLEAKENITTCGAERIC 60
DB 1 MGVHECPAMLWLLSLSLPLGLPVLGAPPRLICDSRVLYERYLLEAKENITTCGAERIC 60
QY 61 SLNENITVPDTKVNPFYAMKMEVGOQAVEWQGLALISEAVLRGQALLVNSSQPMPELQI 120
DB 61 SLNENITVPDTKVNPFYAMKMEVGOQAVEWQGLALISEAVLRGQALLVNSSQPMPELQI 120
QY 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
QY 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
QY 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
DB 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
QY 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
DB 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
QY 241 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTGLHOD 300
DB 241 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTGLHOD 300
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DB 241 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTGLHOD 300
QY 301 WINGKEYKCKVSNKALPASIIEKTIISAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGF 360
DB 301 WINGKEYKCKVSNKALPASIIEKTIISAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGF 360
QY 361 YPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEAL 420
DB 361 YPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEAL 420
QY 421 HNHYYTQKSLSLSPGK 435
DB 421 HNHYYTQKSLSLSPGK 435

RESULT 3

US-11-016-518A-22
; Sequence 22, Application US/11016518A
; Publication No. US20050124045A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
; TITLE OF INVENTION: biological activities
; FILE REFERENCE: 02SUN2004D1
; CURRENT APPLICATION NUMBER: US/11/016,518A
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US 09/932,812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuBPO-L-vfc gamma1 with a 27-amino acid leader peptide (Figure
; OTHER INFORMATION: 2C)
US-11-016-518A-22

Query Match 100.0%; Score 2312; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2e-153;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGVHECPAMLWLLSLSLPLGLPVLGAPPRLICDSRVLYERYLLEAKENITTCGAERIC 60
QY 61 SLNENITVPDTKVNPFYAMKMEVGOQAVEWQGLALISEAVLRGQALLVNSSQPMPELQI 120
DB 61 SLNENITVPDTKVNPFYAMKMEVGOQAVEWQGLALISEAVLRGQALLVNSSQPMPELQI 120
QY 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
QY 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDASAAPLRITTDTPFRKLFRRVSNFLRGKL 180
QY 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
DB 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
QY 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
DB 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVFLFPKPKDITLM 240
QY 241 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTGLHOD 300
DB 241 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTGLHOD 300
QY 241 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTGLHOD 300
DB 241 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTGLHOD 300
QY 301 WINGKEYKCKVSNKALPASIIEKTIISAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGF 360
DB 301 WINGKEYKCKVSNKALPASIIEKTIISAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGF 360
QY 361 YPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEAL 420
DB 361 YPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEAL 420
QY 421 HNHYYTQKSLSLSPGK 435
DB 421 HNHYYTQKSLSLSPGK 435

RESULT 4
US-11-017-185-22
; Sequence 22, Application US/11017185
; Publication No. US20050142642A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001D2

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2006, 08:42:04 ; Search time 41.9037 Seconds

(without alignments)
441.079 Million cell updates/sec

Title: US-10-761-593a-22

Perfect score: 1 MGVECPAMWMLLSLSLP.....MEHALNHVYTKSLSPCK 435

Sequence: 2312

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197.5	95.0	428	7	US-11-029-003-24 Sequence 24, Appl
2	1983.5	85.8	444	7	US-11-029-003-16 Sequence 16, Appl
3	1308.5	56.6	430	7	US-11-029-003-22 Sequence 22, Appl
4	1268.5	54.9	281	6	US-10-841-956a-7 Sequence 7, Appl
5	1263.5	54.6	484	7	US-11-274-910-30 Sequence 30, Appl
6	1255.5	54.3	708	7	US-11-150-533-65 Sequence 65, Appl
7	1241	53.7	255	7	US-11-057-923-24 Sequence 5, Appl
8	1241	53.7	515	6	US-10-954-468-33 Sequence 33, Appl
9	1241	53.7	516	6	US-10-954-468-32 Sequence 32, Appl
10	1241	53.7	518	6	US-10-954-468-31 Sequence 31, Appl
11	1241	53.7	519	6	US-10-954-468-30 Sequence 30, Appl
12	1238	53.5	386	7	US-11-075-047a-58 Sequence 58, Appl
13	1237	53.4	459	6	US-10-949-720-390 Sequence 390, Appl
14	1235.5	53.4	476	7	US-11-274-910-23 Sequence 23, Appl
15	1233	53.3	320	7	US-11-183-205-50 Sequence 50, Appl
16	1230.5	53.2	303	7	US-11-087-719-71 Sequence 71, Appl
17	1229	53.2	270	6	US-10-841-956a-5 Sequence 5, Appl
18	1229	53.2	489	6	US-10-835-475-11 Sequence 11, Appl
19	1229	53.2	514	6	US-10-835-475-11 Sequence 11, Appl
20	1228.5	53.1	467	7	US-11-075-047a-40 Sequence 40, Appl
21	1227	53.1	404	6	US-10-948-053-7 Sequence 7, Appl
22	1226.5	53.0	469	7	US-11-075-047a-38 Sequence 38, Appl
23	1226	53.0	321	7	US-11-186-422-8 Sequence 8, Appl
24	1225	53.0	696	7	US-11-029-003-8 Sequence 8, Appl
25	1224.5	53.0	352	7	US-11-075-047a-34 Sequence 34, Appl

26	1224.5	53.0	452	7	US-11-016-503-6 Sequence 6, Appl
27	1224.5	53.0	455	7	US-11-016-503-14 Sequence 14, Appl
28	1224.5	53.0	455	7	US-11-089-803-4 Sequence 4, Appl
29	1224.5	53.0	455	7	US-11-218-234-4 Sequence 4, Appl
30	1224.5	53.0	455	7	US-11-204-709-10 Sequence 10, Appl
31	1224	52.9	423	7	US-11-029-003-10 Sequence 10, Appl
32	1224	52.9	464	7	US-11-075-047a-42 Sequence 42, Appl
33	1223.5	52.9	473	7	US-11-075-047a-36 Sequence 36, Appl
34	1223	52.9	292	7	US-11-087-719-73 Sequence 73, Appl
35	1223	52.9	292	7	US-11-087-719-75 Sequence 75, Appl
36	1223	52.9	370	7	US-11-075-047a-18 Sequence 18, Appl
37	1223	52.9	455	7	US-11-075-047a-32 Sequence 32, Appl
38	1223	52.9	467	7	US-11-197-488-25 Sequence 25, Appl
39	1223	52.9	480	7	US-11-075-047a-48 Sequence 48, Appl
40	1223	52.9	492	7	US-11-197-488-27 Sequence 27, Appl
41	1223	52.9	572	7	US-11-075-047a-44 Sequence 44, Appl
42	1222.5	52.9	462	7	US-11-016-503-8 Sequence 8, Appl
43	1221.5	52.8	375	7	US-11-075-047a-54 Sequence 54, Appl
44	1221.5	52.8	557	7	US-11-016-503-4 Sequence 4, Appl
45	1221	52.8	251	7	US-11-242-294-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1									
US-11-029-003-24									
Sequence 24, Application US/11029003									
Publication No. US20050260194A1									
GENERAL INFORMATION:									
APPLICANT: PETERS, ROBERT T.									
APPLICANT: MEZO, ADAM R.									
APPLICANT: RIVERA, DANIEL S.									
APPLICANT: BITONTI, ALAN J.									
APPLICANT: STATTEL, JAMES									
TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS									
FILE REFERENCE: 08945.0007-01000									
CURRENT APPLICATION NUMBER: US/11/029,003									
CURRENT FILING DATE: 2005-01-05									
PRIOR APPLICATION NUMBER: 60/539,207									
PRIOR FILING DATE: 2004-01-26									
PRIOR APPLICATION NUMBER: 60/487,964									
PRIOR FILING DATE: 2003-07-17									
PRIOR APPLICATION NUMBER: 60/469,600									
PRIOR FILING DATE: 2003-05-06									
NUMBER OF SEQ ID NOS: 91									
SOFTWARE: PatentIn Ver. 3.2									
SEQ ID NO 24									
LENGTH: 428									
TYPE: PRT									
ORGANISM: Artificial Sequence									
FEATURE:									
OTHER INFORMATION: Description of Artificial Sequence: Synthetic									
OTHER INFORMATION: construct									
US-11-029-003-24									
Query Match									
Best Local Similarity 95.9%; Score 2197.5; DB 7; Length 428;									
Matches 417; Conservative 2; Mismatches 9; Indels 7; Gaps 1;									
QY	1	MGVECPAMWMLLSLSLP	LGPLVGAPRLICDSRVLEKKAENITTCAGHC	60					
DB	1	MGVECPAMWMLLSLSLP	LGPLVGAPRLICDSRVLEKKAENITTCAGHC	60					
QY	61	SLNENITVPTDKVNFYAMKREYVGOAVYWGGLALISEAVLRGALLVNSSQPWEPLQL	120						
DB	61	SLNENITVPTDKVNFYAMKREYVGOAVYWGGLALISEAVLRGALLVNSSQPWEPLQL	120						
QY	121	HYDKAVSGRLSTTLRLAAGAKAISPDAASAPLRTITADTFRKLFRVYSNLRGKL	180						
DB	121	HYDKAVSGRLSTTLRLAAGAKAISPDAASAPLRTITADTFRKLFRVYSNLRGKL	180						
QY	181	KLYTGBACRTDGGSGGSGGGSGGSGGSKDHTHTCPPCPAEVAGBSVFLPPPKDITLM	240						

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Db 181 KYTGACRGTGDE-----FAGAAAVKTHTCPCPAPBELLGGGSVFLFPKPKDTLM 233
Qy 241 ISRTPEVTCVVVDVSHEDPEVKFNNVYDVGVEVNAKTKPREEQYNSTYRVSVLTJVLHOD 300
Db 234 ISRTPEVTCVVVDVSHEDPEVKFNNVYDVGVEVNAKTKPREEQYNSTYRVSVLTJVLHOD 293
Qy 301 MINGEKYCKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGF 360
Db 294 MINGEKYCKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGF 353
Qy 361 YPSDIAVEMESNQGPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRWQGNVFCSVNHEAL 420
Db 354 YPSDIAVEMESNQGPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRWQGNVFCSVNHEAL 413
Qy 421 HNNHYTKSLISPGK 435
Db 414 HNNHYTKSLISPGK 428
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RESULT 2

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US-11-029-003-16
; Sequence 16, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTTEL, JAMES
; TITLE OF INVENTION: IMMUNOLOGICAL CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029, 003
; PRIOR FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539, 207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487, 964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469, 600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-11-029-003-16
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Query Match 85.8%; Score 1983.5; DB 7; Length 444;
Best Local Similarity 85.2%; Pred. No. 3.2e-150;
Matches 399; Conservative 3; Mismatches 20; Indels 45; Gaps 3;
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Qy 7 PAKMLILSLSLPLGAPVIGAPPRICDSRVLEKLEAKENITTCACAHCSLNEN 65
Db 3 PCTLLILAAALPQTGRASRAPRNICDSRVLEKLEAKENITTCACAHCSLNEN 62
Qy 66 ITVPDTRKVFYAKRMKMEVGOAVWOGALLSEAVYRGQALLVNSQPEPQLAVDKA 125
Db 63 ITVPDTRKVFYAKRMKMEVGOAVWOGALLSEAVYRGQALLVNSQPEPQLAVDKA 122
Qy 126 VSGLRSLITLLRALGAKENISPPDAASAPLRTITPTDTRKLFPRVYSNLRGKLYTG 185
Db 123 VSGLRSLITLLRALGAKENISPPDAASAPLRTITPTDTRKLFPRVYSNLRGKLYTG 182
Qy 186 EACRTGDSGGG-----SGGGSGGGSGDKTHTCPCP 217
Db 183 EACRTDREFGGEVQALEKEVAOLEAENQALEKEVAOLEHEGG----- 226
Qy 218 PAEVAVGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNVYDVGVEVNAKT 277
Db 217 PAEVAVGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNVYDVGVEVNAKT 277
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Db 227 PABELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNVYDVGVEVNAKT 286
Qy 278 KPREEQYNSTYRVSVLTJVLHODMNGEKYCKVSNKALPAPIEKTIISKAKQPREPOVY 337
Db 287 KPREEQYNSTYRVSVLTJVLHODMNGEKYCKVSNKALPAPIEKTIISKAKQPREPOVY 346
Qy 338 TLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQGPENNYKTTTPVLDSDGSFPLYSK 397
Db 347 TLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQGPENNYKTTTPVLDSDGSFPLYSK 406
Qy 398 LTVDKSRWQGNVFCSVNHEALHNNHYTKSLISPGK 435
Db 407 LTVDKSRWQGNVFCSVNHEALHNNHYTKSLISPGK 444
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RESULT 3

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US-11-029-003-22
; Sequence 22, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTTEL, JAMES
; TITLE OF INVENTION: IMMUNOLOGICAL CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029, 003
; PRIOR FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539, 207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487, 964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469, 600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-11-029-003-22
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Query Match 56.6%; Score 1308.5; DB 7; Length 430;
Best Local Similarity 63.9%; Pred. No. 1.6e-96;
Matches 265; Conservative 26; Mismatches 57; Indels 67; Gaps 5;
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Qy 40 ERYLLEAKENITTCACAHCSLNENITVPDTRKVFYAKRMKMEVGOAVWOGALLSE 99
Db 64 EEEGNGFOKAEITP---VLHEMIQOIFNLFSTRDSSAADETLIDFTYELVQQLNDLKA 120
Qy 100 AVLRGQALLVNSQPEPQLAVDKAVSGLRSLITLLRALGAKENISPPDAASAPLRT 159
Db 121 CVYQG-----VGVTETPLMEDSILAV----- 142
Qy 160 ITADTRFKLFPRVYSNLRGK-----LKYTGACRGTGDSGGSGG 200
Db 143 -----RKYFQRIITLYLKEKTKYSPCAMEVYVRAIMKSFSLTNLQESLRSKGG-GGSGG 195
Qy 201 GSGGGGSKTHTCPCPAPBELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPE 260
Db 196 GSGGGGSKTHTCPCPAPBELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPE 255
Qy 261 VKENMYVDVGVNAKTKPREEQYNSTYRVSVLTJVLHODMNGEKYCKVSNKALPAPI 320
Db 256 VKENMYVDVGVNAKTKPREEQYNSTYRVSVLTJVLHODMNGEKYCKVSNKALPAPI 315
Qy 321 EKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQGPENNYK 380
Db 316 EKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQGPENNYK 375
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